

Run on: August 17, 2004, 14:23:32 ; Search time 82 Seconds  
 OM nucleic - nucleic search, using sw model

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Title:	US-009-825-489-3			
Scoring table:	IDENTITY_NUC			
Post-processing:	Gapop 10.0 , Gapext 1.0			
Searched:	682709 seqs, 277475446 residues			
Total number of hits satisfying chosen parameters:	1365418			
Minimum DB seq length:	0			
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Database :	Listing first 800 summaries			
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C	255	13.6	68.0	2259	3	US-08-456-108-5	Sequence 5, Appli	328	13.2	66.0	327	4	US-09-428-805-9
C	256	13.6	68.0	2259	3	US-09-265-577-5	Sequence 5, Appli	329	13.2	66.0	352	3	US-08-951-083-127
C	257	13.6	68.0	2259	4	US-09-623-739-5	Sequence 5, Appli	330	13.2	66.0	352	4	US-09-536-784-127
C	258	13.6	68.0	2278	4	US-08-216-428-10	Sequence 10, Appli	331	13.2	66.0	384	4	US-09-543-681A-1889
C	259	13.6	68.0	2587	2	US-08-326-216-3	Sequence 3, Appli	332	13.2	66.0	396	4	US-09-621-976-832
C	260	13.6	68.0	2817	4	US-08-956-117B-295	Sequence 295, App	333	13.2	66.0	430	4	US-09-621-976-8254
C	261	13.6	68.0	2896	3	US-08-930-055A-1	Sequence 1, Appli	340	13.2	66.0	445	4	US-09-621-976-15305
C	262	13.6	68.0	3375	1	US-08-981-931B-1	Sequence 1, Appli	335	13.2	66.0	482	4	US-09-621-976-315
C	263	13.6	68.0	3466	4	US-09-782-906-1	Sequence 1, Appli	341	13.2	66.0	510	4	US-09-003-198A-19
C	264	13.6	68.0	3784	1	US-07-223-033-1	Sequence 1, Appli	342	13.2	66.0	522	4	US-09-598-401C-61
C	265	13.6	68.0	3993	4	US-09-543-681A-3085	Sequence 7, Appli	343	13.2	66.0	495	4	US-09-543-681A-283
C	266	13.6	68.0	4081	3	US-08-999-774A-1	Sequence 7, Appli	339	13.2	66.0	507	3	US-08-761-355-10
C	267	13.6	68.0	4617	4	US-08-930-055A-1	Sequence 1, Appli	340	13.2	66.0	507	4	US-09-003-198A-10
C	268	13.6	68.0	4761	4	US-09-543-681A-1157	Sequence 1157, Ap	341	13.2	66.0	510	4	US-09-134-001C-1698
C	269	13.6	68.0	5024	1	US-08-920-812-7	Sequence 7, Appli	342	13.2	66.0	522	4	US-09-598-401C-61
C	270	13.6	68.0	5024	1	US-08-920-827-7	Sequence 7, Appli	343	13.2	66.0	537	4	US-09-598-401C-63
C	271	13.6	68.0	5024	1	US-08-921-177-7	Sequence 157, App	344	13.2	66.0	538	4	US-08-761-976-2523
C	272	13.6	68.0	5024	1	US-08-342-577C-7	Sequence 7, Appli	345	13.2	66.0	507	4	US-09-003-198A-10
C	273	13.6	68.0	5024	1	US-08-828-828-7	Sequence 1, Appli	346	13.2	66.0	507	4	US-09-428-805-10
C	274	13.6	68.0	5109	4	US-08-930-055A-2	Sequence 1157, Ap	347	13.2	66.0	651	4	US-09-134-001C-1698
C	275	13.6	68.0	5455	1	US-08-342-930-1	Sequence 1, Appli	348	13.2	66.0	688	4	US-09-972-800A-70
C	276	13.6	68.0	6102	4	US-09-524-524-682	Sequence 682, App	349	13.2	66.0	767	4	US-09-524-524-10463
C	277	13.6	68.0	9711	4	US-08-961-577-167	Sequence 157, App	350	13.2	66.0	813	4	US-09-872-733A-19
C	278	13.6	68.0	2055	4	US-08-956-117E-206	Sequence 206, App	351	13.2	66.0	860	4	US-09-621-976-3524
C	279	13.6	68.0	2055	4	US-08-956-117E-206	Sequence 206, App	352	13.2	66.0	870	4	US-09-621-976-3524
C	280	13.6	68.0	31800	4	US-08-311-731A-139	Sequence 139, App	353	13.2	66.0	876	4	US-09-134-000C-860
C	281	13.6	68.0	31769	4	US-08-311-731A-23	Sequence 23, Appli	354	13.2	66.0	885	4	US-09-543-681A-1746
C	282	13.6	68.0	50516	4	US-09-996-336-1	Sequence 1, Appli	355	13.2	66.0	887	4	US-09-247-155-150
C	283	13.6	68.0	50516	3	US-09-338-907-1	Sequence 1, Appli	356	13.2	66.0	899	4	US-09-221-017B-1060
C	284	13.6	68.0	50516	4	US-09-218-287-1	Sequence 1, Appli	357	13.2	66.0	914	4	US-09-673-395A-114
C	285	13.6	68.0	50516	4	US-09-338-907-179	Sequence 179, App	358	13.2	66.0	921	4	US-09-489-039A-1033
C	286	13.6	68.0	50520	4	US-09-218-207-179	Sequence 179, App	359	13.2	66.0	923	4	US-09-221-017B-252
C	287	13.6	68.0	60986	4	US-09-596-002-29	Sequence 29, Appli	360	13.2	66.0	933	4	US-09-107-532A-558
C	288	13.6	68.0	39900	4	US-10-027-933-11	Sequence 11, Appli	361	13.2	66.0	951	4	US-09-543-681A-2787
C	289	13.6	68.0	4403765	3	US-09-103-4040A-2	Sequence 2, Appli	362	13.2	66.0	969	4	US-09-543-681A-3696
C	290	13.6	68.0	4411529	3	US-09-103-2940A-1	Sequence 1, Appli	363	13.2	66.0	1002	4	US-09-641-638B-583
C	291	13.6	68.0	4411526	4	US-09-113-294A-1855	Sequence 1855, Ap	364	13.2	66.0	1007	4	US-09-620-312D-817
C	292	13.6	68.0	4411526	4	US-09-663-17-15	Sequence 15, Appli	365	13.2	66.0	1021	4	US-09-956-17E-14
C	293	13.6	68.0	4431	4	US-09-621-916-1686	Sequence 16186, A	366	13.2	66.0	1035	4	US-09-134-001C-687
C	294	13.6	68.0	4432	4	US-09-071-055-443	Sequence 443, App	367	13.2	66.0	1092	4	US-09-543-681A-2787
C	295	13.6	68.0	453	4	US-08-817-441-64	Sequence 64, Appli	368	13.2	66.0	1113	4	US-09-540-236-338
C	296	13.6	68.0	453	4	US-08-071-055-441	Sequence 441, App	369	13.2	66.0	1116	3	US-08-916-443A-16
C	297	13.6	68.0	6308	4	US-08-222-719-16	Sequence 16, Appli	370	13.2	66.0	1142	4	US-09-936-165A-92
C	298	13.6	68.0	6311	4	US-08-470-925-16	Sequence 16, Appli	371	13.2	66.0	1233	3	US-08-853-839-1
C	299	13.6	68.0	6319	4	US-08-471-613-16	Sequence 16, Appli	372	13.2	66.0	1239	4	US-09-252-991A-1224
C	300	13.6	68.0	6338	5	US-09-539-333-1043-16	Sequence 16, Appli	373	13.2	66.0	1242	4	US-09-543-681A-1921
C	301	13.6	68.0	6390	4	US-09-134-000C-1299	Sequence 1299, App	374	13.2	66.0	1248	2	US-08-897-340-5
C	302	13.6	68.0	6406	4	US-08-556-171B-427	Sequence 427, App	375	13.2	66.0	1248	3	US-09-252-329-5
C	303	13.6	68.0	6473	3	US-08-907-700-6	Sequence 6, Appli	376	13.2	66.0	1291	1	US-08-952-755-2
C	304	13.6	68.0	2616	4	US-09-107-532A-2573	Sequence 2573, Ap	377	13.2	66.0	1291	1	US-08-443-679-2
C	305	13.6	68.0	2715	4	US-08-954-631A-313	Sequence 313, App	378	13.2	66.0	1308	4	US-09-205-258-215
C	306	13.6	68.0	3001	4	US-09-539-333-213	Sequence 16, Appli	379	13.2	66.0	1429	2	US-08-244-205-6
C	307	13.6	68.0	3279	4	US-09-275-688-1	Sequence 1299, App	380	13.2	66.0	1429	2	US-08-876-585-2
C	308	13.6	68.0	4123	4	US-08-620-312D-379	Sequence 441, App	381	13.2	66.0	1429	2	US-08-776-585-1
C	309	13.6	68.0	4695	4	US-09-620-312D-379	Sequence 1, Appli	382	13.2	66.0	1404	4	US-08-489-039A-4718
C	310	13.6	68.0	4697	4	US-09-963-137-131	Sequence 333, App	383	13.2	66.0	1414	4	US-09-442-296B-9
C	311	13.6	68.0	4700	4	US-09-620-312D-333	Sequence 3, Appli	384	13.2	66.0	1429	2	US-08-244-205-6
C	312	13.6	68.0	4707	4	US-08-147-717-23	Sequence 16, Appli	385	13.2	66.0	1429	2	US-08-244-205-6
C	313	13.6	68.0	4939	5	PCT-US3-0385-3	Sequence 1, Appli	386	13.2	66.0	1429	5	PCT-US92-10284-6
C	314	13.6	68.0	4939	3	US-09-700-755-12	Sequence 12, Appli	387	13.2	66.0	1429	5	PCT-US92-10284-8
C	315	13.6	68.0	4939	3	US-09-231-839-12	Sequence 1, Appli	388	13.2	66.0	1455	4	US-08-489-039A-4800
C	316	13.6	68.0	51952	3	US-08-947-823-1	Sequence 1, Appli	389	13.2	66.0	1457	4	US-09-673-395A-554
C	317	13.6	68.0	53165	4	US-09-214-881-1	Sequence 1, Appli	390	13.2	66.0	1479	4	US-09-489-039A-1847
C	318	13.6	68.0	578431	4	US-09-551-339-3	Sequence 1, Appli	391	13.2	66.0	1482	3	US-08-994-441B-69
C	319	13.6	68.0	66.0	20	US-09-972-800A-58	Sequence 58, Appli	392	13.2	66.0	1482	3	US-08-993-722A-69



C	539	13.2	66.0	1959	4	US-09-427-769-9	Sequence 9, Appli	612	13.2	66.0	4505	5	PCT-US95-12642-13	
C	540	13.2	66.0	1959	4	US-09-427-769-11	Sequence 11, Appli	613	13.2	66.0	4525	4	US-09-424-283-7	
C	541	13.2	66.0	1959	4	US-09-427-769-13	Sequence 13, Appli	614	13.2	66.0	4645	4	US-09-485-286-14	
C	542	13.2	66.0	1959	4	US-09-427-769-27	Sequence 17, Appli	615	13.2	66.0	4700	2	US-09-928-692-16	
C	543	13.2	66.0	1959	4	US-09-427-769-29	Sequence 29, Appli	616	13.2	66.0	4700	4	US-09-339-972-16	
C	544	13.2	66.0	1959	4	US-09-427-769-39	Sequence 39, Appli	C	617	13.2	66.0	4771	2	US-09-865-650-2
C	545	13.2	66.0	1959	4	US-09-427-769-41	Sequence 41, Appli	C	618	13.2	66.0	4771	3	US-09-240-473-2
C	546	13.2	66.0	1959	4	US-09-427-769-43	Sequence 43, Appli	C	619	13.2	66.0	4864	4	US-09-340-798A-1
C	547	13.2	66.0	1959	4	US-09-427-769-45	Sequence 45, Appli	C	620	13.2	66.0	4915	4	US-09-173-053-7
C	548	13.2	66.0	1959	4	US-09-427-769-47	Sequence 47, Appli	C	621	13.2	66.0	4928	1	US-09-345-913-1
C	549	13.2	66.0	1959	4	US-09-427-769-49	Sequence 49, Appli	C	622	13.2	66.0	4928	3	US-09-811-562-1
C	550	13.2	66.0	1959	4	US-09-427-769-53	Sequence 53, Appli	C	623	13.2	66.0	4928	4	US-09-628-445-1
C	551	13.2	66.0	1959	4	US-09-427-769-56	Sequence 63, Appli	C	624	13.2	66.0	4965	2	US-09-564-313-1
C	552	13.2	66.0	1959	4	US-09-427-769-65	Sequence 65, Appli	C	625	13.2	66.0	4965	3	PCT-US94-06069-1
C	553	13.2	66.0	1959	4	US-09-427-769-67	Sequence 67, Appli	C	626	13.2	66.0	5053	4	US-09-311-784A-35
C	554	13.2	66.0	1959	4	US-09-427-769-97	Sequence 97, Appli	C	627	13.2	66.0	5053	3	US-09-039-955B-18
C	555	13.2	66.0	1970	3	US-08-687-590-56	Sequence 56, Appli	C	628	13.2	66.0	5183	4	US-09-811-562-1
C	556	13.2	66.0	1972	6	5187-911-1	Patent No. 5187-911	C	629	13.2	66.0	5203	4	US-09-811-562-1
C	557	13.2	66.0	1978	4	US-09-525-223A-8	Sequence 8, Appli	C	630	13.2	66.0	5215	4	US-09-173-053-8
C	558	13.2	66.0	1981	4	US-09-647-390-17	Sequence 17, Appli	C	631	13.2	66.0	5243	2	US-09-414-335-2
C	559	13.2	66.0	1981	4	US-09-173-027-276	Sequence 27, Appli	C	632	13.2	66.0	5502	4	US-09-703-705-785
C	560	13.2	66.0	2115	1	US-08-329-681A-3	Sequence 3, Appli	C	633	13.2	66.0	5502	4	US-09-736-457-785
C	561	13.2	66.0	2280	3	US-08-996-441B-102	Sequence 102, App	C	634	13.2	66.0	5502	4	US-09-671-325-785
C	562	13.2	66.0	2280	3	US-08-993-722-02	Sequence 102, App	C	635	13.2	66.0	5502	4	US-09-671-325-785
C	563	13.2	66.0	2280	3	US-08-993-170A-102	Sequence 102, App	C	636	13.2	66.0	5502	4	US-09-589-184-785
C	564	13.2	66.0	2280	3	US-08-993-775B-102	Sequence 102, App	C	637	13.2	66.0	5592	4	US-09-495-797-37
C	565	13.2	66.0	2280	4	US-09-620-312D-559	Sequence 102, App	C	638	13.2	66.0	5845	4	US-09-703-173-053-1
C	566	13.2	66.0	2280	4	US-09-543-601A-3143	Sequence 102, App	C	639	13.2	66.0	5862	2	US-08-663-998-4
C	567	13.2	66.0	2392	4	US-09-797-664A-1	Sequence 1, Appli	C	640	13.2	66.0	5838	2	US-08-850-880-3
C	568	13.2	66.0	2430	5	PCT-US92-00040-1	Sequence 1, Appli	C	641	13.2	66.0	5838	2	US-08-941-616-3
C	569	13.2	66.0	2479	3	US-09-050-863-4	Sequence 4, Appli	C	642	13.2	66.0	5838	2	US-08-814-877-3
C	570	13.2	66.0	2479	4	US-09-359-081-4	Sequence 4, Appli	C	643	13.2	66.0	5838	4	US-09-272-432A-3
C	571	13.2	66.0	2622	4	US-09-543-601A-3143	Sequence 559, App	C	644	13.2	66.0	5899	4	US-08-663-998-3
C	572	13.2	66.0	2624	4	US-09-370-838-19	Sequence 3143, App	C	645	13.2	66.0	5899	4	US-08-173-053-2
C	573	13.2	66.0	2632	3	US-08-329-92B-32	Sequence 3143, App	C	646	13.2	66.0	5902	4	US-08-941-989-4
C	574	13.2	66.0	2632	3	US-08-329-92B-32	Sequence 32, Appli	C	647	13.2	66.0	5902	4	US-08-381-989-4
C	575	13.2	66.0	2885	4	US-10-164-595-39	Sequence 32, Appli	C	648	13.2	66.0	5926	4	US-09-027-169-3
C	576	13.2	66.0	3224	3	US-08-965-729A-3	Sequence 39, Appli	C	649	13.2	66.0	5926	4	US-09-027-169-4
C	577	13.2	66.0	3224	3	US-08-965-729A-3	Sequence 4, Appli	C	650	13.2	66.0	5952	5	PCT-US95-12642-17
C	578	13.2	66.0	3311	4	US-10-164-595-11	Sequence 1, Appli	C	651	13.2	66.0	6044	1	US-08-316-950-18
C	579	13.2	66.0	3356	1	US-08-246-403A-1	Sequence 1, Appli	C	652	13.2	66.0	6044	5	PCT-US95-12642-18
C	580	13.2	66.0	3356	4	US-08-246-403A-4	Sequence 4, Appli	C	653	13.2	66.0	6047	1	US-08-950-10-12
C	581	13.2	66.0	3375	4	US-09-309-572-1	Sequence 1, Appli	C	654	13.2	66.0	6047	5	PCT-US95-12642-12
C	582	13.2	66.0	3375	4	US-09-718-096-1	Sequence 1, Appli	C	655	13.2	66.0	6171	1	US-08-316-950-17
C	583	13.2	66.0	3418	2	US-08-944-916-12	Sequence 12, Appli	C	656	13.2	66.0	6171	1	US-08-950-17-1
C	584	13.2	66.0	3424	4	US-09-553-690-3	Sequence 3, Appli	C	657	13.2	66.0	6353	4	US-09-702-705-784
C	585	13.2	66.0	3470	4	US-09-976-594-345	Sequence 345, App	C	658	13.2	66.0	6353	4	US-09-736-457-784
C	586	13.2	66.0	3474	4	US-09-340-798A-43	Sequence 43, Appli	C	659	13.2	66.0	6353	4	US-09-614-124B-784
C	587	13.2	66.0	3610	4	US-09-194-949A-1	Sequence 1, Appli	C	660	13.2	66.0	6353	4	US-09-671-325-784
C	588	13.2	66.0	3870	2	US-08-853-659A-2	Sequence 26, Appli	C	661	13.2	66.0	6353	4	US-09-589-184-784
C	589	13.2	66.0	3895	4	US-08-961-527-201	Sequence 201, App	C	662	13.2	66.0	6407	1	US-07-977-630-1
C	590	13.2	66.0	3987	4	US-08-082-649B-83	Sequence 83, Appli	C	663	13.2	66.0	6407	1	US-07-977-630-2
C	591	13.2	66.0	3987	4	US-08-07-977-630-20	Sequence 345, App	C	664	13.2	66.0	6873	3	US-08-131-028A-1
C	592	13.2	66.0	3993	1	US-08-136-955-14	Sequence 14, Appli	C	665	13.2	66.0	6873	3	US-08-131-028A-8
C	593	13.2	66.0	3993	5	PCT-US95-12642-14	Sequence 14, Appli	C	666	13.2	66.0	6978	4	US-08-872-733A-15
C	594	13.2	66.0	4059	2	PCT-US95-12642-11	Sequence 2, Appli	C	667	13.2	66.0	7091	3	US-08-975-762-46
C	595	13.2	66.0	4059	5	PCT-US95-12642-11	Sequence 2, Appli	C	668	13.2	66.0	7091	3	US-09-295-028-46
C	596	13.2	66.0	4066	3	US-09-298-367B-3	Sequence 3, Appli	C	669	13.2	66.0	7091	4	US-09-106-582-46
C	597	13.2	66.0	4120	1	US-07-977-630-21	Sequence 20, Appli	C	670	13.2	66.0	7091	4	US-09-159-469-46
C	598	13.2	66.0	4120	1	US-07-977-630-21	Sequence 21, Appli	C	671	13.2	66.0	7091	4	US-09-691-542-46
C	599	13.2	66.0	4120	1	US-08-316-950-11	Sequence 21, Appli	C	672	13.2	66.0	7091	4	US-09-872-733A-15
C	600	13.2	66.0	4120	1	US-08-316-950-11	Sequence 21, Appli	C	673	13.2	66.0	7641	1	US-07-924-028A-5
C	601	13.2	66.0	4202	4	US-09-483-19-2	Sequence 2, Appli	C	674	13.2	66.0	7676	4	US-09-556-213-21
C	602	13.2	66.0	4261	4	US-08-194-949A-25	Sequence 3, Appli	C	675	13.2	66.0	7676	4	US-09-072-596-208
C	603	13.2	66.0	4296	5	PCT-US95-12642-15	Sequence 15, Appli	C	676	13.2	66.0	7676	4	US-03-072-967-213
C	604	13.2	66.0	4326	3	US-08-760-615-7	Sequence 16, Appli	C	677	13.2	66.0	7676	4	US-09-281-849-9
C	605	13.2	66.0	4338	1	US-08-015-966A-1	Sequence 17, Appli	C	678	13.2	66.0	8031	4	US-09-643-597-254
C	606	13.2	66.0	4338	2	US-08-015-966A-1	Sequence 18, Appli	C	679	13.2	66.0	8031	4	US-09-884-884A-254
C	607	13.2	66.0	4352	1	US-08-316-950-16	Sequence 19, Appli	C	680	13.2	66.0	8031	4	US-09-541-615A-254
C	608	13.2	66.0	4352	5	PCT-US95-12642-16	Sequence 20, Appli	C	681	13.2	66.0	8031	4	US-09-606-421B-254
C	609	13.2	66.0	4352	5	PCT-US95-12642-16	Sequence 21, Appli	C	682	13.2	66.0	8366	4	US-08-872-733A-6
C	610	13.2	66.0	4427	3	US-08-312-953-2	Sequence 22, Appli	C	683	13.2	66.0	8430	3	US-09-131-028A-10
C	611	13.2	66.0	4505	1	US-08-311-028A-10	Sequence 23, Appli	C	684	13.2	66.0	8430	3	US-09-131-028A-10

c	c	685	13.2	66.0	8501	3	US-08-733-901-1	758	12.8	64.0	301	4	US-09-703-705-1714
c	c	686	13.2	66.0	8967	2	US-08-653-652A-6	759	12.8	64.0	301	4	US-09-736-457-1714
c	c	687	13.2	66.0	8967	2	US-08-653-652A-9	760	12.8	64.0	301	4	US-09-717-325-1714
c	c	688	13.2	66.0	8967	2	US-08-653-652A-64	761	12.8	64.0	304	4	US-09-439-261-4
c	c	689	13.2	66.0	9067	2	US-08-653-652A-67	762	12.8	64.0	304	4	US-09-227-613-4
c	c	690	13.2	66.0	90254	4	US-08-911-527-29	763	12.8	64.0	304	4	US-09-250-609-100
c	c	691	13.2	66.0	10317	3	US-09-058-746-1	765	12.8	64.0	354	4	US-09-250-611-100
c	c	692	13.2	66.0	10317	3	US-09-418-142-1	765	12.8	64.0	357	4	US-09-107-532A-93
c	c	693	13.2	66.0	10323	4	US-09-280-28A-11	766	12.8	64.0	396	4	US-09-161-173-93
c	c	694	13.2	66.0	10324	4	US-08-876-991-1	767	12.8	64.0	395	4	US-09-713-550-153
c	c	695	13.2	66.0	10284	2	US-08-909-853-1	768	12.8	64.0	414	4	US-09-621-976-1843
c	c	696	13.2	66.0	12284	2	US-09-059-853-1	769	12.8	64.0	425	4	US-09-221-017B-344
c	c	697	13.2	66.0	12311	3	US-08-750-717-1	770	12.8	64.0	425	4	US-09-250-609-101
c	c	698	13.2	66.0	12665	4	US-08-901-521-134	771	12.8	64.0	425	4	US-09-250-611-101
c	c	699	13.2	66.0	12785	4	US-08-591-691-1	772	12.8	64.0	449	4	US-09-429-755-211
c	c	700	13.2	66.0	14113	3	US-09-223-134-1	773	12.8	64.0	454	3	US-09-991-789A-211
c	c	701	13.2	66.0	14113	3	US-08-932-801-1	774	12.8	64.0	454	4	US-09-062-451-211
c	c	702	13.2	66.0	14113	3	US-08-233-531-1	775	12.8	64.0	454	4	US-09-589-326-211
c	c	703	13.2	66.0	14194	4	US-09-577-424-3	776	12.8	64.0	454	4	US-09-289-198-211
c	c	704	13.2	66.0	15538	4	US-09-534-337-1	777	12.8	64.0	454	4	US-09-429-755-211
c	c	705	13.2	66.0	15538	4	US-08-439-461-3	778	12.8	64.0	477	4	US-09-711-550-197
c	c	706	13.2	66.0	15846	3	US-07-830-609-3	779	12.8	64.0	454	3	US-09-991-789A-211
c	c	707	13.2	66.0	15846	2	US-08-846-762-1	780	12.8	64.0	487	4	US-09-439-313-206
c	c	708	13.2	66.0	15846	2	US-08-833-659A-2	781	12.8	64.0	487	4	US-09-534-616A-206
c	c	709	13.2	66.0	15846	2	US-08-833-659A-3	782	12.8	64.0	487	4	US-09-232-149A-206
c	c	710	13.2	66.0	15846	2	US-08-833-659A-60	783	12.8	64.0	487	4	US-09-159-812-206
c	c	711	13.2	66.0	15846	2	US-08-833-659A-61	784	12.8	64.0	487	4	US-09-429-755-211
c	c	712	13.2	66.0	15846	4	US-09-316-40A-1	785	12.8	64.0	487	4	US-09-711-550-197
c	c	713	13.2	66.0	15846	4	US-09-839-993-3	786	12.8	64.0	487	4	US-09-991-789A-211
c	c	714	13.2	66.0	15846	4	US-10-133-295-3	787	12.8	64.0	487	4	US-09-589-326-211
c	c	715	13.2	66.0	15846	4	US-09-657-346A-96	788	12.8	64.0	495	4	US-09-232-149A-206
c	c	716	13.2	66.0	15846	4	US-08-311-731A-136	789	12.8	64.0	501	4	US-09-134-000C-205
c	c	717	13.2	66.0	15846	4	US-08-311-731A-26	790	12.8	64.0	504	4	US-09-636-215-206
c	c	718	13.2	66.0	15846	4	US-09-750-580-1	791	12.8	64.0	516	4	US-09-250-609-99
c	c	719	13.2	66.0	15846	4	US-09-791-211-10	792	12.8	64.0	516	4	US-09-250-611-99
c	c	720	13.2	66.0	15846	4	US-09-536-002-39	793	12.8	64.0	516	4	US-09-541-681A-299
c	c	721	13.2	66.0	15846	4	US-09-651-596A-76	794	12.8	64.0	527	4	US-09-621-976-1248
c	c	722	13.2	66.0	15846	4	US-09-913-514-1	795	12.8	64.0	540	4	US-09-134-000C-240
c	c	723	13.2	66.0	15846	4	US-09-913-514-2	796	12.8	64.0	558	4	US-09-328-352-240
c	c	724	13.2	66.0	15846	4	US-09-497-858A-38	797	12.8	64.0	586	4	US-09-918-681-17
c	c	725	13.2	66.0	15846	4	US-09-676-610A-24	798	12.8	64.0	601	4	US-09-465-559-21
c	c	726	13.2	66.0	15846	4	US-09-877-177A-10	799	12.8	64.0	645	4	US-09-465-171B-686
c	c	727	13.2	66.0	15846	4	US-09-586-002-41	800	12.8	64.0	651	4	US-09-328-352-2818
c	c	728	13.2	66.0	15846	4	US-08-316-421B-1						
c	c	729	13.2	66.0	15846	4	US-09-317-787-221						
c	c	730	13.2	66.0	15846	4	US-09-621-976-19085						
c	c	731	13.2	66.0	15846	4	US-09-338-352-3803						
c	c	732	13.2	66.0	15846	4	US-09-357-3844						
c	c	733	13.2	66.0	15846	2	US-08-536-117-8						
c	c	734	13.2	66.0	15846	4	US-09-620-312D-735						
c	c	735	13.2	66.0	15846	3	US-09-382-256-9						
c	c	736	13.2	66.0	15846	3	US-09-395-115-9						
c	c	737	13.2	66.0	15846	4	US-09-416-265-9						
c	c	738	13.2	66.0	15846	4	US-09-676-187-9						
c	c	739	13.2	66.0	15846	2	US-08-696-944-1						
c	c	740	13.2	66.0	15846	4	US-09-543-681A-86						
c	c	741	13.2	66.0	15846	3	US-09-330-537-3						
c	c	742	13.2	66.0	15846	1	US-08-330-537-4						
c	c	743	13.2	66.0	15846	1	US-08-137-252-2						
c	c	744	13.2	66.0	15846	4	US-09-620-312D-226						
c	c	745	13.2	66.0	15846	4	US-08-956-171B-67						
c	c	746	13.2	66.0	15846	4	US-09-801-876-3						
c	c	747	13.2	66.0	15846	4	US-10-254-869-3						
c	c	748	13.2	66.0	15846	2	US-09-422-978-9320						
c	c	749	13.2	66.0	15846	4	US-09-404-879-345						
c	c	750	13.2	66.0	15846	2	US-052-991A-5226						
c	c	751	13.2	66.0	15846	4	US-09-543-681A-32278						
c	c	752	13.2	66.0	15846	3	US-09-172-108-35						
c	c	753	13.2	66.0	15846	3	US-09-172-711-33						
c	c	754	13.2	66.0	15846	4	US-09-313-294-1666						
c	c	755	13.2	66.0	15846	4	US-09-489-039A-6634						
c	c	756	13.2	66.0	15846	4	US-09-394-294A-1178						
c	c	757	13.2	66.0	15846	4	US-09-313-294A-4029						
Sequence 1	Appli	Sequence 1	Appli	Sequence 1	Appli	Sequence 1	Appli	Sequence 1	Appli	Sequence 1	Appli	Sequence 1	Appli
Sequence 2	Appli	Sequence 2	Appli	Sequence 2	Appli	Sequence 2	Appli	Sequence 2	Appli	Sequence 2	Appli	Sequence 2	Appli
Sequence 3	Appli	Sequence 3	Appli	Sequence 3	Appli	Sequence 3	Appli	Sequence 3	Appli	Sequence 3	Appli	Sequence 3	Appli
Sequence 4	Appli	Sequence 4	Appli	Sequence 4	Appli	Sequence 4	Appli	Sequence 4	Appli	Sequence 4	Appli	Sequence 4	Appli
Sequence 5	Appli	Sequence 5	Appli	Sequence 5	Appli	Sequence 5	Appli	Sequence 5	Appli	Sequence 5	Appli	Sequence 5	Appli
Sequence 6	Appli	Sequence 6	Appli	Sequence 6	Appli	Sequence 6	Appli	Sequence 6	Appli	Sequence 6	Appli	Sequence 6	Appli
Sequence 7	Appli	Sequence 7	Appli	Sequence 7	Appli	Sequence 7	Appli	Sequence 7	Appli	Sequence 7	Appli	Sequence 7	Appli
Sequence 8	Appli	Sequence 8	Appli	Sequence 8	Appli	Sequence 8	Appli	Sequence 8	Appli	Sequence 8	Appli	Sequence 8	Appli
GENERAL INFORMATION:													
APPLICANT:	MCCUTCHEON, SANDRA												
APPLICANT:	LAWRENCE LIVERMORE NATIONAL LABORATORY												
TITLE OF INVENTION:	DETECTION AND QUANTITATION OF POLYMORPHISMS, DNA SEQUENCE VARIATIONS, AND NUCLEIC ACID MISMATCHES												
TITLE OF INVENTION:	DNA DAMAGE AND DNA MISMATCH												
FILE REFERENCE:	IL-10689												
CURRENT APPLICATION NUMBER:	US-091651,656												
CURRENT FILING DATE:	2000-08-29												
PRIOR APPLICATION NUMBER:	60192,764												
PRIOR FILING DATE:	2000-03-28												
NUMBER OF SEQ ID NO:	106												
SEQ ID NO:	8												
LENGTH:	822												
ALIGNMENTS													
RESULT 1													
US-09-651-656-8/c													
SEQUENCE 8: Application US/09651656													
PATENT NO: 6340566													
ORGANISM: Homo sapiens													
US-09-651-656-8													
Query Match	100.0%	Score	20	DB	4	Best	Local Similarity	100.0%	Pred.	No.	0.48;	Length:	822

ALIGNMENTS

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCATCTCATGTTGATG 20

Db 743 GGTCATCTCATGTTGATG 724

RESULT 2

US-09-650-855-8/C

; Sequence 8, Application US/09650855

; Patent No. 6365355

; GENERAL INFORMATION:

; APPLICANT: MCCUTCHEON-MALONEY, SANDRA

; LAWRENCE BERKELEY NATIONAL LABORATORY

; TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA

; TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA

; TITLE OF INVENTION: MISMATCHES

; FILE REFERENCE: II-1-084

CURRENT APPLICATION NUMBER: US/09/650, 855

CURRENT FILING DATE: 2000-08-29

PRIOR APPLICATION NUMBER: 60/1192, 764

PRIOR FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 106

SEQ ID NO 8

LENGTH: 822

TYPE: DNA

ORGANISM: Homo sapiens

US-09-650-855-8

Query Match 100%; Score 20; DB 4; Length 822;

Best Local Similarity 100.0%; Pred. No. 0.48;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCATCTCATGTTGATG 20

Db 743 GGTCATCTCATGTTGATG 724

RESULT 3

US-08-961-527-40/C

; Sequence 40, Application US/08961527

; Patent No. 6420135

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII TEXT

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: P8340P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

RESULT 4

US-09-385-982-62

; Sequence 62, Application US/09385982

; Patent No. 6262334

; GENERAL INFORMATION:

; APPLICANT: ENDEGE, WILSON O., ET AL.

; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

; FILE REFERENCE: CDDNA-260XX

CURRENT APPLICATION NUMBER: US/09/385, 982

CURRENT FILING DATE: 1999-08-30

EARLIER APPLICATION NUMBER: 09/328, 111

EARLIER FILING DATE: 1998-06-08

EARLIER APPLICATION NUMBER: 60/117, 393

EARLIER FILING DATE: 1999-01-27

EARLIER APPLICATION NUMBER: 60/098, 639

EARLIER FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 544

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 62

LENGTH: 614

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: misc\_feature

NAME/KEY: misc\_feature

LOCATION: (1)..(614)

OTHER INFORMATION: n = A,T,C or G

US-09-385-982-62

Query Match 79.0%; Score 15.8; DB 3; Length 614;

Best Local Similarity 89.5%; Pred. No. 60;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCCATCTCATGTTGATG 20

Db 466 GTCCATCTCATGTTGATG 484

RESULT 5

US-09-023-655-1225/C

; Sequence 1225, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cooks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1500

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/023,655  
 FILING DATE: HEREWITH  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0001 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-5555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 1225:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 686 base pairs  
 TYPE: nucleic acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: 9246741

US-09-023-655-1225

Query Match 79.0%; Score 15.8; DB 4; Length 686;  
 Best Local Similarity 89.5%; Pred. No. 61; Mismatches 0;  
 Matches 17; Conservative 0; Indels 0; Gaps 0;

QY 1 GGTCCATCTCTGTTGAT 19  
 Db 628 GGTCCATCTCTGTTGAT 610

RESULT 6  
 US-09-543-681A-137/c  
 ; Sequence 137, Application US/09543681A  
 ; Patent No. 6505709  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GARY BRETON  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
 ; FILE REFERENCE: 2709\_1.002-001  
 ; CURRENT APPLICATION NUMBER: US/09/543,681A  
 ; CURRENT FILING DATE: 2000-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/128,706  
 ; PRIOR FILING DATE: 1999-04-09  
 ; NUMBER OF SEQ ID NOS: 8344  
 ; SEQ ID NO 137  
 ; LENGTH: 801  
 ; TYPE: DNA  
 ; ORGANISM: Proteus mirabilis  
 ; US-09-543-681A-137

Query Match 79.0%; Score 15.8; DB 4; Length 801;  
 Best Local Similarity 89.5%; Pred. No. 62; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGCCATCTCTGTTGAT 20  
 Db 136 GACCAAATCTCTGTTGAT 118

RESULT 9  
 US-08-956-171E-1137  
 ; Sequence 1137, Application US/08956171E  
 ; Patent No. 6593114  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Charles Kunisch  
 ; Gil H. Choi  
 ; Patrick S. Dillon  
 ; Craig A. Rosen  
 ; Steven C. Barish  
 ; Michael R. Fannon  
 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
 ; NUMBER OF SEQUENCES: 5256  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville

RESULT 7  
 US-09-543-681A-1773/c  
 ; Sequence 1773, Application US/09543681A  
 ; Patent No. 6605709

STATE: Maryland ; Sequence 2478, Application US/09328352  
 ZIP: 20550 ; Patent No. 6362958  
 COMPUTER READABLE FORM: ; GENERAL INFORMATION:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage ; APPLICANT: Gary L. Breton et al.  
 COMPUTER: HP Vectra 486/33 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
 OPERATING SYSTEM: MSDOS version 6.2 ; FILE REFERENCE: GTC99-03PA  
 SOFTWARE: ASCII Text ; CURRENT APPLICATION NUMBER: US/09/328, 352  
 CURRENT APPLICATION DATA: ; CURRENT FILING DATE: 1999-06-04  
 APPLICATION NUMBER: US/08/956, 171E ; NUMBER OF SEQ ID NOS: 8252  
 FILING DATE: 20-Oct-1997 ; SEQ ID NO: 2478  
 CLASSIFICATION: <Unknown> ; LENGTH: 4884  
 PRIORITY APPLICATION DATA: ; TYPE: DNA  
 APPLICATION NUMBER: 60/009, 861 ; ORGANISM: Acinetobacter baumannii  
 FILING DATE: January 5, 1996 ; US-09-328-352-2478  
 APPLICATION NUMBER: 08/781, 986  
 FILING DATE: January 3, 1997  
 ATTORNEY/AGENT INFORMATION: ;  
 NAME: Mark J. Hyman  
 REFERENCE/DOCKET NUMBER: PB248P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (240) 314-1224  
 TELEX: (301) 309-8439  
 INFORMATION FOR SEQ ID NO: 1137:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1137:  
 LENGTH: 330 base pairs ;  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 ;  
 ; US-08-956-171E-1137  
 ;  
 ; Query Match 76.0%; Score 15.2; DB 4; Length 330;  
 ; Best Local Similarity 85.0%; Pred. No. 1.1e+02;  
 ; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 ;  
 ; Qy 1 GGTCCTAATCTGTGATG 20  
 ; Db 284 GGACCAAACTCTGGGATG 303  
 ;  
 ;  
 RESULT 10 ;  
 US-09-489-039A-5224/c ; Sequence 1, Application US/09328352  
 ; Sequence 5224, Application US/09328352  
 ; Patent No. 6362958 ;  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Gary Breton et. al ;  
 ; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR  
 ;  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ;  
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
 ;  
 ; FILE REFERENCE: 2709, 2004001  
 ;  
 ; CURRENT APPLICATION NUMBER: US/09/489, 039A  
 ;  
 ; CURRENT FILING DATE: 2000-01-27  
 ;  
 ; PRIORITY APPLICATION NUMBER: US 60/117, 747  
 ;  
 ; PRIORITY FILING DATE: 1999-01-29  
 ;  
 ; NUMBER OF SEQ ID NOS: 14342  
 ;  
 ; SEQ ID NO 5224  
 ;  
 ; LENGTH: 1419  
 ;  
 ; TYPE: DNA  
 ;  
 ; ORGANISM: Klebsiella pneumoniae  
 ;  
 ; US-09-489-039A-5224  
 ;  
 ;  
 ; Query Match 76.0%; Score 15.2; DB 4; Length 1419;  
 ; Best Local Similarity 85.0%; Pred. No. 1.1e+02;  
 ; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 ;  
 ; Qy 1 GGTCCTAATCTGTGATG 20  
 ; Db 487 GGTCCTAATCTGTGATGCTG 468  
 ;  
 ;  
 ; RESULT 11  
 ;  
 ; US-09-328-352-2478

LOCATION: 2946..3632  
 FEATURE: CDS  
 NAME/KEY: CDS  
 LOCATION: 3774..5306  
 FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 5429..11755  
 ; US-08-646-695-1  
 Query Match 76.0%; Score 15.2; DB 3; Length 14311;  
 Best Local Similarity 85.0%; Pred. No. 2e+02; Mismatches 3; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 GGTCATCACTCATGTTGATG 20  
 Db 11703 GGTCATCACTCATGTTGAG 11722  
 RESULT 13  
 US-08-646-695-7/C  
 ; Sequence 7, Application US/08646695  
 ; Patent No. 6168943  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rose, John K.  
 ; TITLE OF INVENTION: RECOMBINANT VESICULOVIRUSES AND THEIR  
 ; TITLE OF INVENTION: USES  
 ; NUMBER OF SEQUENCES: 44  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 115 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patient Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/06053  
 FILING DATE: 01-MAY-1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mirock, S. Leslie  
 REGISTRATION NUMBER: 10,872  
 REFERENCE/DOCKET NUMBER: 6523-009-228  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-9090  
 TELEX: (212) 869-9741/8864  
 TELEX: 66141 PENNIE  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14311 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 760..2028  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 2092..2889  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 2946..3635  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 3774..5309  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 5429..11758  
 ; PCT-US96-06053-1  
 Query Match 76.0%; Score 15.2; DB 5; Length 14311;  
 Best Local Similarity 85.0%; Pred. No. 2e+02; Mismatches 3; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 GGTCATCACTCATGTTGATG 20  
 Db 11703 GGTCATCACTCATGTTGAG 11722  
 RESULT 14  
 PCT-US96-06053-1  
 ; Sequence 1, Application PC/TUS9606053  
 ; GENERAL INFORMATION:  
 ;  
 ; ADDRESSEE: PENNIE & EDMONDS  
 ; STREET: 115 Avenue of the Americas  
 ; CITY: New York

STATE: New York  
 COUNTRY: USA  
 ZIP: 10036-2711  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US96/06053  
 FILING DATE: 01-MAY-1996  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Misrock, S. Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 6523-009-228  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 790-0909  
 TELEX/FAX: (212) 869-9741/8864  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 14311 base pairs  
 STRANDEDNESS: double  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 PCT-US96-06053-7

RESULT 16  
 Query Match 76.0%; Score 15.2; DB 5; Length 14311;  
 Best Local Similarity 85.0%; Pred. No. 2.e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCCATACTCATGTCATG 20  
 Db 2609 GGCTCTTACATGATGAG 2590

---

RESULT 17  
 US-09-198-452A-1/c  
 Sequence 1, Application US/09198452A  
 Patent No. 6559294  
 GENERAL INFORMATION:  
 APPLICANT: Griffais, R.  
 TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection  
 TITLE OF INVENTION: and treatment of infection  
 FILE REFERENCE: 9710-003-999  
 CURRENT APPLICATION NUMBER: US/09/198,452A  
 CURRENT FILING DATE: 1998-11-24  
 NUMBER OF SEQ ID NOS: 6849  
 SEQ ID NO 1  
 LENGTH: 1230025

TYPE: DNA  
 ORGANISM: Chlamydia pneumoniae  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)..(15000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (15001)..(30000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (30001)..(45000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (45001)..(60000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (60001)..(75000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (75001)..(90000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (90001)..(105000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (105001)..(120000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (120001)..(135000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (135001)..(150000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (150001)..(165000)  
 OTHER INFORMATION: n=a or c or g or t  
 NAME/KEY: misc feature  
 LOCATION: (165001)..(180000)  
 OTHER INFORMATION: n=a or c or g or t

RESULT 18  
 US-08-311-731A-132  
 Sequence 132, Application US/08311731A  
 Patent No. 6583265  
 GENERAL INFORMATION:  
 APPLICANT: SMITH, DOUGLAS  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES  
 TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 411  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
 STREET: 600 ATLANTIC AVENUE  
 CITY: BOSTON  
 STATE: MASSACHUSETTS  
 COUNTRY: USA  
 ZIP: 02110

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/311,731A  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GATES, EDWARD R.  
 REGISTRATION NUMBER: 31,616  
 REFERENCE/DOCKET NUMBER: C0044/7125  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/720-3500  
 TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 132:

LOCATION: (165001)..(180000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (180001)..(195000)  
LOCATION: (195001)..(210000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (210001)..(225000)  
LOCATION: (225001)..(240000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (240001)..(255000)  
LOCATION: (255001)..(270000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (270001)..(285000)  
LOCATION: (285001)..(300000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (300001)..(315000)  
LOCATION: (315001)..(330000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (330001)..(345000)  
LOCATION: (345001)..(360000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (360001)..(375000)  
LOCATION: (375001)..(390000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (390001)..(405000)  
LOCATION: (405001)..(420000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (420001)..(435000)  
LOCATION: (435001)..(450000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (450001)..(465000)  
LOCATION: (465001)..(480000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (480001)..(495000)  
LOCATION: (495001)..(510000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (510001)..(525000)  
LOCATION: (525001)..(540000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (540001)..(555000)  
LOCATION: (555001)..(570000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (570001)..(585000)  
LOCATION: (585001)..(600000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (600001)..(615000)  
LOCATION: (615001)..(630000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (630001)..(645000)  
LOCATION: (645001)..(660000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (660001)..(675000)  
LOCATION: (675001)..(690000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (690001)..(705000)  
LOCATION: (705001)..(720000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (720001)..(735000)  
LOCATION: (735001)..(750000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (750001)..(765000)  
LOCATION: (765001)..(780000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (780001)..(795000)  
LOCATION: (795001)..(810000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (810001)..(825000)  
LOCATION: (825001)..(840000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (840001)..(855000)  
LOCATION: (855001)..(870000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (870001)..(885000)  
LOCATION: (885001)..(900000) OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature LOCATION: (900001)..(915000)

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; NAME/KEY: misc_feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc_feature

Query Match    76.0%: Score 15.2; DB 4; Length 1230025;
Best Local Similarity 85.0%; Pred. No. 2.7e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 GGTCCATACTCATGTTGATG 20
Db      175246 GGGCGTCTCTGTTGATG 175227

RESULT 18
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; US-09-103-840A-2

Query Match    76.0%: Score 15.2; DB 3; Length 4403765;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 GGTCCATACTCATGTTGATG 20
Db      2185302 GGTCCAGACTCANGGGATG 2185283

RESULT 19
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6224328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
; US-09-103-840A-1

Query Match    76.0%: Score 15.2; DB 3; Length 4411529;

Best Local Similarity 85.0%; Pred. No. 1.2e+02; Mismatches 3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy      1 GGTCCATACTCATGTTGATG 20
Db      2188003 GGTCCAGACTCATGGGATG 2187984

RESULT 20
US-09-328-352-1128
; Sequence 1128, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTCG9-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1128
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-1128

Query Match    74.0%: Score 14.8; DB 4; Length 315;
Best Local Similarity 88.9%; Pred. No. 1.7e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      3 TCCATACATGTTGATG 20
Db      263 TCTATAGTCATGTTGATG 280

RESULT 21
US-09-328-352-1227/c
; Sequence 1227, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTCG9-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1227
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-1227

Query Match    74.0%: Score 14.8; DB 4; Length 348;
Best Local Similarity 88.9%; Pred. No. 1.7e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      3 TCCATACATGTTGATG 20
Db      305 TCTATAGTCATGTTGATG 288

RESULT 22
US-09-621-976-3741
; Sequence 3741, Application US/09621976
; General Information:
; Applicant: Dumas Milne Edwards, J.B.
; Applicant: Jobert, S.
; Applicant: Giordano, J.Y.
; Title of Invention: ESTs and Encoded Human Proteins.
; File Reference: GENSET-054PR2
; Current Application Number: US/09/621,976

Query Match    76.0%: Score 15.2; DB 3; Length 4411529;

```

CURRENT FILING DATE: 2000-07-21  
 NUMBER OF SEQ ID NOS: 19335  
 SOFTWARE: Patent.pm  
 SEQ ID NO 3741  
 LENGTH: 387  
 ;  
 ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; LOCATION: 191..376  
 US-09-621-976-3741  
 Query Match 74.0%; Score 14.8; DB 4; Length 387;  
 Best Local Similarity 88.9%; Pred. No. 1.8e+02; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 3 TCCATACATCACTGTGATG 20  
 Db 182 TCCAGACTCATGATGATG 199  
 ;  
 RESULT 23  
 US-09-328-352-992  
 ; Sequence 992, Application US/09338352  
 ; Patent No. 6562958  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary L. Breton et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACCINETOBACTER  
 ; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: GRIC9-03PA  
 ; CURRENT APPLICATION NUMBER: US/09/328,352  
 ; CURRENT FILING DATE: 1999-06-04  
 ; NUMBER OF SEQ ID NOS: 8252  
 ; SEQ ID NO 992  
 ; LENGTH: 546  
 ;  
 ; ORGANISM: Acinetobacter baumannii  
 ; TYPE: DNA  
 ;  
 US-09-328-352-992  
 Query Match 74.0%; Score 14.8; DB 4; Length 546;  
 Best Local Similarity 88.9%; Pred. No. 1.9e+02; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 3 TCCATACATCACTGTGATG 20  
 Db 10 TCTATAGTCATGTGATG 27  
 ;  
 RESULT 24  
 US-09-489-039A-911  
 ; Sequence 911, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Bretton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; FILE REFERENCE: 2709-2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489,039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIORITY APPLICATION NUMBER: US 60/117,747  
 ; PRIORITY FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 911  
 ; LENGTH: 2244  
 ;  
 ; TYPE: DNA  
 ;  
 US-09-489-039A-911  
 Query Match 72.0%; Score 14.4; DB 4; Length 2244;  
 Best Local Similarity 93.8%; Pred. No. 3.7e+02; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 CATACTCATGTGATG 20  
 Db 969 CATGCCTCATGTGATG 954  
 ;  
 RESULT 25  
 US-09-489-039A-953  
 ; Sequence 953, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; FILE REFERENCE: 2709-2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489,039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIORITY APPLICATION NUMBER: -US 60/117,747  
 ; PRIORITY FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 953  
 ; LENGTH: 2310  
 ;  
 ; ORGANISM: Klebsiella pneumoniae  
 ; TYPE: DNA  
 ;  
 US-09-489-039A-953  
 Query Match 72.0%; Score 14.4; DB 4; Length 2310;  
 Best Local Similarity 93.8%; Pred. No. 3.7e+02; Gaps 0;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 CATACTCATGTGATG 20  
 Db 969 CATGCCTCATGTGATG 954  
 ;  
 RESULT 26  
 US-08-136-743B-40  
 ; Sequence 40, Application US/08136743B  
 ; Patent No. 5459063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barry S. Cooperman, Harvey Rubin,  
 ; APPLICANT: Jerome Salem, and Alison L. Fisher  
 ; TITLE OF INVENTION: "Plasmodium falciparum Ribonucleic Acid Reductase, DNA Sequences Therefor and Peptide Inhibitor"  
 ; TITLE OF INVENTION: cleoTide Reductase, DNA Sequences Therefor and Peptide Inhibit  
 ; NUMBER OF SEQUENCES: 67  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: The University of Pennsylvania  
 ; STREET: Suite 330  
 ; STREET: 3700 Market Street  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19104-3246  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION NUMBER: US/08/136,743B  
 ; APPLICATION NUMBER: DATA: US/08/136,743B  
 ; FILING DATE: 10/14/93  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Monaco, Daniel A.  
 ; REGISTRATION NUMBER: 30,480  
 ; REFERENCE/DOCKET NUMBER: 3957-10  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-8383  
 ; TELEFAX: (215) 568-5449  
 ; TELEX: No. 5459033e  
 ; INFORMATION FOR SEQ ID NO: 40:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2433 nucleotides  
 ;  
 ; TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-136-743B-3
; Sequence 3, Application US/08136743B
; Patent No. 5459063
; GENERAL INFORMATION:
; APPLICANT: Barry S. Cooperman, Harvey Rubin,
; TITLE OF INVENTION: "Plasmodium falciparum Ribonucleotide Reductase, DNA Sequences Therefor and Peptide Inhibitor"
; TITLE OF INVENTION: "Thereof"
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The University of Pennsylvania
; STREET: Suite 330
; STREET: 3700 Market Street
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19104-3246
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,743B
; FILING DATE: 10/14/93
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REGISTRATION NUMBER: 30,480
; REFERENCE/DOCKET NUMBER: 3057-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEX: No. 5459063E
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2663 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-136-743B-3

Query Match 2 GTCCATCTCTGTTG 72.0%; Score 14.4; DB 1; Length 2663;
Best Local Similarity 93.8%; Pred. No. 3.8e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GTCCATCTCTGTTG 17
Db 2499 GTGGATCTCATGTG 2514

RESULT 28
US-08-247-901C-1
; Sequence 1, Application US/08247901C
; Patent No. 5750384
; GENERAL INFORMATION:
; APPLICANT: Jacobs et al
; TITLE OF INVENTION: L5 SHUTTLE PHASMIDS
;
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RESULT 29  
 US-09-075-904-1  
 Sequence 1, Application US/09075904  
 ;  
 GENERAL INFORMATION:  
 APPLICANT: Jacobs, et al.  
 TITLE OF INVENTION: L5 SHUTTLE PHASMDs  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amster, Rothstein & Ebenstein  
 STREET: 90 Park Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10016  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Word Processor (ASCII)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/075, 904  
 FILING DATE: May 11, 1998  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/247, 901  
 FILING DATE: May 23, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Bogbian, Elizabeth A  
 REGISTRATION NUMBER: 39,911  
 REFERENCE/DOCKET NUMBER: 96700/475  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 697-5995  
 TELEX: TWX 710-581-4766  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 50341  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: L5 shuttle Phasmid sequence  
 DESCRIPTION: L5 shuttle Phasmid sequence  
 HYPOTHETICAL: NO  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM: L5 mycobacteriophage  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 POSITION IN GENOME:  
 CHROMOSOME SEGMENT:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:

RESULT 30  
 US-09-075-904-1  
 Sequence 1, Application US/09426436  
 ;  
 Patent No. 6225066  
 GENERAL INFORMATION:  
 APPLICANT: William R. Jacobs, Jr.  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Barry R. Bloom  
 REGISTRATION NUMBER: 39,911  
 REFERENCE/DOCKET NUMBER: 96700/475  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 286-0954 or 286-0082  
 TELEX: TWX 710-581-4766  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 50341  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: L5 shuttle Phasmid sequence  
 DESCRIPTION: L5 shuttle Phasmid sequence  
 HYPOTHETICAL: NO  
 ANTI-SENSE:  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM: L5 mycobacteriophage  
 STRAIN:  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 POSITION IN GENOME:  
 CHROMOSOME SEGMENT:  
 FEATURE:  
 NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS:  
 TITLE:

Query Match 72.0%; Score 14.4; DB 2; Length 50341;  
 Best Local Similarity 93.8%; Pred. No. 6e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Document Number: 15;  
 Publication Date: 1998-05-11;  
 Relevant Residues in Seq ID No: US-09-075-904-1

JOURNAL: PAGES: VOLUME:  
 DATE: DOCUMENT NUMBER: FILING DATE:  
 PUBLICATION DATE: RELEVANT RESIDUES IN SEQ ID NO:

ORGANISM: mycobacteriophage L5  
 STRAIN: not applicable  
 INDIVIDUAL ISOLATE: L5  
 DEVELOPMENTAL STAGE: not applicable  
 HAPLOTYPE: not applicable  
 TISSUE TYPE: not applicable  
 CELL TYPE: not applicable  
 CELL LINE: not applicable  
 ORGANELLE: not applicable  
 IMMEDIATE SOURCE: mycobacteriophage L5 particles  
 POSITION IN GENOME: entire genome

FEATURE: NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS: Hattull and Sarkis  
 TITLE: DNA Sequence, Structure and Gene Expression of Mycobacteriophage L5:  
 TITLE: A Phage System for Mycobacterial Genetics  
 JOURNAL: Molecular Microbiology  
 VOLUME: 7  
 PAGES: 395-405  
 DATE: 1993

US-09-426-436-1

Query Match 72.0%; Score 14.4; DB 3; Length 52297;  
 Best Local Similarity 93.8%; Pred. No. 6e+02; Mismatches 15; Conservative 0; Indels 0; Gaps 0; Matches 15;

Qy 5 CATACTCATGTGATG 20  
 Db 9132 CATCCTCATGTGATG 9147

RESULT 31

US-08-705-557-1  
 ; Sequence 1, Application US/08705557  
 ; Patent No. 6300061  
 ; GENERAL INFORMATION:  
 APPLICANT: William R. Jacobs, Jr.  
 APPLICANT: Barry R. Bloom  
 APPLICANT: Graham F. Hattull  
 TITLE OF INVENTION: MYCOBACTERIAL SPECIES-SPECIFIC TITLE OF INVENTION: REPORTER MYCOBACTERIOPHAGES NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amster, Rothstein & Ebenstein  
 STREET: 90 Park Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10016

COMPUTER READABLE FORM:  
 COMPUTER TYPE: 3.5 inch 1.44 Mb storage diskette  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: Word Processor (ASCII)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/057,557  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/057,531  
 FILING DATE:  
 APPLICATION NUMBER: 07/033,431  
 FILING DATE: February 7, 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pasqualini, Patricia A.  
 REGISTRATION NUMBER: 34,894  
 REFERENCE/DOCKET NUMBER: 96700/238

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 697-5995  
 TELEFAX: (212) 286-0854 or 286-0082  
 TELEX: TWX 71-581-4766 1:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 52297  
 TYPE: nucleotide  
 STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE:  
 DESCRIPTION: phage genome sequence  
 HYPOTHETICAL: no  
 ANTI-SENSE: no  
 FRAGMENT TYPE: not applicable.  
 ORIGINAL SOURCE:  
 ORGANISM: mycobacteriophage L5  
 INDIVIDUAL ISOLATE: L5  
 DEVELOPMENTAL STAGE: not applicable  
 HAPLOTYPE: not applicable  
 TISSUE TYPE: not applicable  
 CELL TYPE: not applicable  
 CELL LINE: not applicable  
 ORGANELLE: not applicable  
 IMMEDIATE SOURCE: mycobacteriophage L5 particles  
 POSITION IN GENOME: entire genome

FEATURE: NAME/KEY:  
 LOCATION:  
 IDENTIFICATION METHOD:  
 OTHER INFORMATION:  
 PUBLICATION INFORMATION:  
 AUTHORS: Hattull and Sarkis  
 TITLE: DNA Sequence, Structure and Gene Expression of Mycobacteriophage L5:  
 TITLE: A Phage System for Mycobacterial Genetics  
 JOURNAL: Molecular Microbiology  
 VOLUME: 7  
 PAGES: 395-405  
 DATE: 1993

US-08-705-557-1

Query Match 72.0%; Score 14.4; DB 4; Length 52297;  
 Best Local Similarity 93.8%; Pred. No. 6e+02; Mismatches 15; Conservative 0; Indels 0; Gaps 0; Matches 15;

Qy 5 CATACTCATGTGATG 20  
 Db 9132 CATCCTCATGTGATG 9147

RESULT 32

US-09-135-782-10  
 ; Sequence 10, Application US/09135782  
 ; Patent No. 6027929  
 ; GENERAL INFORMATION:  
 APPLICANT: Xu, Shuang-Yong  
 TITLE OF INVENTION: Method For Cloning And Producing The NSPI Restriction Endonuclease Endonuclease  
 TITLE OF INVENTION: Endonuclease In *E. coli* And Purification Of The NSPI Restriction Endonuclease  
 TITLE OF INVENTION: Recombinant NSPI Restriction Endonuclease  
 FILE REFERENCE: NBB-143  
 CURRENT APPLICATION NUMBER: US/09/135,782  
 CURRENT FILING DATE: 1998-08-18  
 NUMBER OF SEQ ID NOS: 10  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 10  
 LENGTH: 36  
 TYPE: DNA  
 ORGANISM: No. 6027929toc sp.

US-09-135-782-10

Query Match ; Score 14.2; DB 3; Length 36;  
 Best Local Similarity 84.2%; Pred. No. 2.4e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGTCATCATCTCAGTGTGAT 19  
 Db 5 GATCCATCATCTCAGTGTGAT 23

RESULT 33  
 US-08-956-171E-986  
 ; Sequence 986, Application US/08956171E  
 Patent No. 6533114

GENERAL INFORMATION:  
 APPLICANT: Charles Kunisch  
 Gil R. Choi  
 Patrick S. Dillon  
 Steven C. Barash  
 Michael R. Fannon  
 Craig A. Rosen

TITLE OF INVENTION: staphylococcus aureus Polynucleotides and Sequences  
 NUMBER OF SEQUENCES: 5256  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Disquette, 3.50 inch, 1.4Mb storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MSBOS version 6.2  
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/956, 171E  
 FILING DATE: 20-10-1997  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/009, 861  
 FILING DATE: January 5, 1996  
 APPLICATION NUMBER: 08/781, 986  
 FILING DATE: January 3, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mark J. Hyman  
 REGISTRATION NUMBER: 46, 789  
 REFERENCE/DOCKET NUMBER: PB248P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (240) 314-1224  
 TELEFAX: (301) 309-8439  
 INFORMATION FOR SEQ ID NO: 986:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 329 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 986:  
 US-08-956-171E-986

RESULT 34  
 US-09-134-001C-2448  
 ; Sequence 2448, Application US/09134001C  
 Patent No. 6380370

GENERAL INFORMATION:  
 NUMBER OF SEQ ID NOS: 5674

SEQ ID NO: 2448  
 LENGTH: 378  
 TYPE: DNA  
 ORGANISM: Staphylococcus epidermidis  
 US-09-134-001C-2448

Query Match ; Score 14.2; DB 4; Length 378;  
 Best Local Similarity 84.2%; Pred. No. 3.5e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GTCCATCATCTCAGTGTGAT 20  
 Db 193 GACCATCATCTCAGTGTGAT 175

RESULT 35  
 US-09-252-991A-11719  
 ; Sequence 11719, Application US/09252991A  
 ; Patent No. 6551795

GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252, 991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074, 788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094, 190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO: 11719  
 LENGTH: 423  
 TYPE: DNA  
 ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-11719

Query Match ; Score 14.2; DB 4; Length 423;  
 Best Local Similarity 84.2%; Pred. No. 3.5e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GTCCATCATCTCAGTGTGAT 20  
 Db 77 GRCGATCGTCATGTGGATG 95

RESULT 36  
 US-09-252-991A-13151  
 ; Sequence 13151, Application US/09252991A  
 ; Patent No. 6551795

GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252, 991A  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074, 788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094, 190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142

RESULT 37  
 US-09-134-001C-2448/c  
 ; Sequence 2448, Application US/09134001C  
 Patent No. 6380370

GENERAL INFORMATION:

RESULT 37  
 Query Match 71.0%; Score 14.2; DB 4; Length 483;  
 Best Local Similarity 84.2%; Pred. No. 3.7e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 1 GGTCCATACATGTTGAT 19  
 Db 26 GATCCATGGTCATGTTGAT 44

RESULT 37  
 US-09-134-000C-244  
 ; Sequence 244, Application US/09134000C  
 ; Patent No. 6517156  
 GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 TITLE OF INVENTION: ENTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS  
 CURRENT APPLICATION NUMBER: US/09/134, 000C  
 CURRENT FILING DATE: 1998-08-13  
 PRIOR APPLICATION NUMBER: US 60/055, 778  
 PRIOR FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 244  
 LENGTH: 510  
 TYPE: DNA  
 ORGANISM: Enterococcus faecalis  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (330)..(491)  
 OTHER INFORMATION: Nucleotides 330, 382, 430, 440, 449 & 491 are "n" wherein  
 OTHER INFORMATION: "n" = any nucleotide.  
 US-09-134-000C-244

Query Match 71.0%; Score 14.2; DB 4; Length 510;  
 Best Local Similarity 84.2%; Pred. No. 3.7e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 GTGCCATACTCATGTTGAT 20  
 Db 187 GTGCCATACTCATGTTGAT 205

RESULT 38  
 US-09-107-532A-735  
 ; Sequence 735, Application US/09107532A  
 ; Patent No. 653275  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A Doucette-Stamm and David Bush  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 TITLE OF INVENTION: ENTEROCOCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02354  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:

RESULT 39  
 US-09-342-681C-1/C  
 Sequence 11, Application US/09342681C  
 ; Patent No. 6355782  
 GENERAL INFORMATION:  
 APPLICANT: Zonana et al.  
 TITLE OF INVENTION: Hyposyndactyly ectodermal dysplasia genes and proteins  
 CURRENT APPLICATION NUMBER: US/09/342, 681C  
 CURRENT FILING DATE: 1999-06-29  
 PRIOR APPLICATION NUMBER: 60/092, 279  
 PRIOR FILING DATE: 1998-07-09  
 PRIOR APPLICATION NUMBER: 60/112, 366  
 PRIOR FILING DATE: 1998-12-15  
 NUMBER OF SEQ ID NOS: 123  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 11  
 LENGTH: 743  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (302)..(302)  
 OTHER INFORMATION: n represents a, c, t, or g  
 US-09-342-681C-11

Query Match 71.0%; Score 14.2; DB 4; Length 743;  
 Best Local Similarity 84.2%; Pred. No. 3.9e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 GTGCCATACTCATGTTGAT 20  
 Db 538 GGTCTTGCTCATGTTGAT 520

RESULT 40  
US-09-252-991A-9153/c  
; Sequence 9153, Application US/09252991A  
; Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/1252, 991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074, 788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094, 190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 9153  
LENGTH: 909  
; ORGANISM: *Pseudomonas aeruginosa*  
; US-09-252-991A-9153

RESULT 41  
US-09-634-238-121  
; Sequence 121, Application US/0964238  
; Patent No. 654472  
GENERAL INFORMATION:  
APPLICANT: Glenn, Matthew  
APPLICANT: Havukkala, Ilkka J.  
APPLICANT: Bloksberg, Leonard, N.  
APPLICANT: Lubbers, Mark W.  
APPLICANT: Dekker, James  
APPLICANT: Christensson, Anna C.  
APPLICANT: Holland, Ross  
APPLICANT: O'Toole, Paul W.  
APPLICANT: Reid, Julian R.  
APPLICANT: Coolbear, Timothy  
TITLE OF INVENTION: Polynucleotides, materials incorporating them and methods for using them.  
TITLE OF INVENTION: them and methods for using them.  
FILE REFERENCE: 11000 104301  
CURRENT APPLICATION NUMBER: US/09/634, 238  
CURRENT FILING DATE: 2000-08-08  
NUMBER OF SEQ ID NOS: 422  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 121  
LENGTH: 1065  
; TYPE: DNA  
; ORGANISM: *Lactobacillus rhamnosus*  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1065)  
; OTHER INFORMATION: n = A,T,C or G  
; US-09-634-238-121

Query Match  
Best Local Similarity 84.2%; Pred. No. 4.2e+02; DB 4; Length 1065;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 42  
US-09-342-681C-14/c  
; Sequence 14, Application US/09342681C  
; Patent No. 6355782  
GENERAL INFORMATION:  
APPLICANT: Zonana et al.  
TITLE OF INVENTION: Hypohidrotic ectodermal dysplasia genes and proteins  
FILE REFERENCE: 52978  
CURRENT APPLICATION NUMBER: US/09/342, 681C  
CURRENT FILING DATE: 1999-06-29  
PRIOR APPLICATION NUMBER: 60/032, 279  
PRIOR FILING DATE: 1998-07-09  
PRIOR APPLICATION NUMBER: 60/112, 366  
PRIOR FILING DATE: 1998-12-15  
NUMBER OF SEQ ID NOS: 123  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 14  
LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: *Homo sapiens*  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1176)  
; US-09-342-681C-14

Query Match  
Best Local Similarity 84.2%; Pred. No. 4.2e+02; DB 4; Length 1176;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 43  
US-09-252-991A-11577/c  
; Sequence 11577, Application US/09252991A  
; Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252, 991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074, 788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094, 190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 11577  
LENGTH: 1185  
; TYPE: DNA  
; ORGANISM: *Pseudomonas aeruginosa*  
; US-09-252-991A-11577

Query Match  
Best Local Similarity 84.2%; Pred. No. 4.2e+02; DB 4; Length 1185;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 44  
US-08-286-020-1  
; Sequence 1, Application US/08286020  
; Patent No. 5339095  
GENERAL INFORMATION:  
APPLICANT: Macombe B. Sticklen and Ravindra K. Hajela  
; TITLE OF INVENTION: A Chitinase cDNA Clone From a

TITLE OF INVENTION: Disease Resistant American Elm Tree  
 TITLE OF INVENTION: Elm Tree  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ian C. McLeod  
 STREET: 2190 Commons Parkway  
 CITY: Okemos  
 STATE: Michigan  
 COUNTRY: USA  
 ZIP: 48864  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
 COMPUTER: Acer  
 OPERATING SYSTEM: MS-DOS 5.00  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/286,020  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ian C. McLeod  
 REGISTRATION NUMBER: 20,931  
 REFERENCE/DOCKET NUMBER: MSU 4.1-207  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 347-4100  
 TELEX: (517) 347-4103  
 TELEFAX: No. 5239095e  
 INFORMATION FOR SEQ ID NO: 1:  
 LENGTH: 1225  
 SEQUENCE CHARACTERISTICS:  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: DNA  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM: Ulmus Americana  
 STRAIN: NPS 3-487  
 INDIVIDUAL ISOLATE: N/A  
 DEVELOPMENTAL STAGE: N/A  
 HAPLOTYPE: N/A  
 ORGANELLE: N/A  
 IMMEDIATE SOURCE: N/A  
 POSITION IN GENOME: N/A  
 FEATURE:  
 NAME/KEY: chitinase encoding DNA  
 LOCATION:  
 IDENTIFICATION METHOD: sequencing  
 OTHER INFORMATION: DNA needed for chitinase  
 OTHER INFORMATION: in elm.  
 PUBLICATION INFORMATION:  
 US-08-286-020-1

Query Match 71.0%; Score 14.2; DB 1; Length 1225;  
 Best Local Similarity 84.2%; Pred. No. 4.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCCATCTACTGTTGAT 19  
 Db 517 GGTCCTAATCTTGGGAT 535

RESULT 45  
 US-08-603-919-1  
 ; Sequence 1, Application US/08603919

Patent No. 5728382  
 GENERAL INFORMATION:  
 APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela  
 TITLE OF INVENTION: A Chitinase cDNA Clone From a  
 TITLE OF INVENTION: Disease Resistant American Elm Tree  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ian C. McLeod  
 STREET: 2190 Commons Parkway  
 CITY: Okemos  
 STATE: Michigan  
 ZIP: 48864  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage  
 COMPUTER: Acer  
 OPERATING SYSTEM: MS-DOS 5.00  
 SOFTWARE: Wordperfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/603,919  
 FILING DATE:  
 CLASSIFICATION: 536  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ian C. McLeod  
 REGISTRATION NUMBER: 20,931  
 REFERENCE/DOCKET NUMBER: MSU 4.1-207  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 347-4100  
 TELEX: No. 5728382e  
 INFORMATION FOR SEQ ID NO: 1:  
 LENGTH: 1225  
 SEQUENCE CHARACTERISTICS:  
 TYPE: Nucleic Acid  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE: DNA  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM: Ulmus Americana  
 STRAIN: NPS 3-487  
 INDIVIDUAL ISOLATE: N/A  
 DEVELOPMENTAL STAGE: N/A  
 HAPLOTYPE: N/A  
 TISSUE TYPE: N/A  
 CELL TYPE: N/A  
 CELL LINE: N/A  
 IMMEDIATE SOURCE: N/A  
 POSITION IN GENOME: N/A  
 FEATURE:  
 NAME/KEY: chitinase encoding DNA  
 LOCATION:  
 IDENTIFICATION METHOD: sequencing  
 OTHER INFORMATION: DNA needed for chitinase  
 OTHER INFORMATION: in elm.  
 PUBLICATION INFORMATION:  
 US-08-603-919-1

Query Match 71.0%; Score 14.2; DB 1; Length 1225;  
 Best Local Similarity 84.2%; Pred. No. 4.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCCATCTACTGTTGAT 19  
 Db 517 GGTCCTAATCTTGGGAT 535



INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1315 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: N  
 ANTI-SENSE: N

US-09-519-489-8

Query Match 71.0%; Score 14.2; DB 4; Length 1315;  
 Best Local Similarity 84.2%; Pred. No. 4.3e+02;  
 Matches 16; Conservative 0; Mismatches 3;  
 Indels 0; Gaps 0;

Qy	2	GTCCATACTCATGTGATG	20
Db	805	GTCCCCACTGATGTTGATG	787

RESULT 49

US-09-252-991A-11863

; Sequence 11863; Application US/09252991A

; Patent No. 6551795

GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenstein et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196\_136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 11863

LENGTH: 1396

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-11863

Query Match 71.0%; Score 14.2; DB 4; Length 1386;  
 Best Local Similarity 84.2%; Pred. No. 4.3e+02;  
 Matches 16; Conservative 0; Mismatches 3;  
 Indels 0; Gaps 0;

Qy 2 GTCCATACTCATGTGATG 20

Db 1248 GTCCATCGTCATGGATG 1266

RESULT 50

US-09-489-039A-3739

; Sequence 3739; Application US/09489039A

; Patent No. 6510836

GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709\_2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 3739

LENGTH: 1398

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-3739

Query Match 71.0%; Score 14.2; DB 4; Length 1398;  
 Best Local Similarity 84.2%; Pred. No. 4.4e+02;

	Matches	16;	Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	2	GTCCATACTCATGTGATG	20							
Db	433	GTCCGACTCATGTCATG	451							

Search completed: August 17, 2004, 15:46:45

Job time : 126 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: August 17, 2004, 15:02:58 ; Search time 362 Seconds  
(without alignments)

US-09-825-489-3  
271.083 Million cell updates/sec

Title: US-09-825-489-3  
Perfect score: 20  
Sequence: 1 ggccatactcatgtgtatg 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 245303834 residues  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 800 summaries

Database : Published Applications NA:\*

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19: /cgnd\_6/prodata/2/pbpna/us60\_PUBCOMB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

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2	20	100.0	486	9 US-09-867-701-754 Sequence 754, Appli
3	20	100.0	506	9 US-09-867-701-217 Sequence 2117, Appli
4	20	100.0	513	9 US-09-867-701-2107 Sequence 2117, Appli
5	20	100.0	1377	11 US-09-825-489-13 Sequence 13, Appli
6	20	100.0	1407	15 US-10-103-313-116 Sequence 116, Appli
7	20	100.0	14670	15 US-10-101-310-1587 Sequence 587, Appli
8	17	85.0	1526	13 US-10-027-632-257254 Sequence 257254, Appli
9	17	85.0	1526	16 US-10-027-632-257254 Sequence 257254, Appli
10	16.8	84.0	1473	13 US-10-158-444-40 Sequence 40, Appli
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12	16.4	82.0	1049	16 US-10-027-632-253417 Sequence 253417, Appli
13	15.8	79.0	238	13 US-10-085-40734 Sequence 40734, A
14	15.8	79.0	238	16 US-10-242-335A-40734 Sequence 40734, A

c 15 15.8 79.0 296 12 US-09-733-627A-2949 Sequence 2949, APP  
c 16 15.8 79.0 431 15 US-10-60-036-3118 Sequence 3118, APP  
c 17 15.8 79.0 462 10 US-03-918-995-12216 Sequence 12216, APP  
c 18 15.8 79.0 540 13 US-10-085-783A-45577 Sequence 45577, APP  
c 19 15.8 79.0 540 16 US-10-242-535A-45577 Sequence 62, APP  
c 20 15.8 79.0 614 10 US-09-871-161-62 Sequence 1225, APP  
c 21 15.8 79.0 686 17 US-10-641-643-1225 Sequence 20394, APP  
c 22 15.8 79.0 765 13 US-10-424-599-20394 Sequence 64375, APP  
c 23 15.8 79.0 789 17 US-10-437-963-64475 Sequence 7531, APP  
c 24 15.8 79.0 1329 17 US-10-437-963-7531 Sequence 7531, APP  
c 25 15.8 79.0 3021 12 US-10-041-018-111 Sequence 111, APP  
c 26 15.8 79.0 5874 12 US-10-041-018-112 Sequence 112, APP  
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c 28 15.4 77.0 519 13 US-10-027-632-79848 Sequence 79848, APP  
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c 31 15.4 77.0 519 16 US-10-027-632-79849 Sequence 79849, APP  
c 32 15.4 77.0 551 9 US-09-764-847-497 Sequence 497, APP  
c 33 15.4 77.0 551 15 US-10-092-154-497 Sequence 66708, APP  
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c 35 15.4 77.0 553 16 US-10-021-632-311196 Sequence 311196, APP  
c 36 15.4 77.0 573 13 US-10-027-632-311195 Sequence 311195, APP  
c 37 15.4 77.0 573 13 US-10-021-632-311197 Sequence 311197, APP  
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c 47 15.2 76.0 292 13 US-09-424-599-127062 Sequence 127062, APP  
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c 49 15.2 76.0 330 13 US-10-329-624-1137 Sequence 1137, APP  
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c 51 15.2 76.0 449 17 US-10-437-963-31302 Sequence 31302, APP  
c 52 15.2 76.0 464 13 US-10-424-599-90875 Sequence 90875, APP  
c 53 15.2 76.0 469 13 US-10-424-599-90875 Sequence 32729, APP  
c 54 15.2 76.0 572 13 US-10-027-632-208409 Sequence 208409, APP  
c 55 15.2 76.0 572 16 US-10-027-632-208409 Sequence 208409, APP  
c 56 15.2 76.0 606 17 US-10-437-963-55289 Sequence 55289, APP  
c 57 15.2 76.0 630 13 US-10-424-599-128976 Sequence 128976, APP  
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c 59 15.2 76.0 1107 13 US-10-424-599-12729 Sequence 218, APP  
c 60 15.2 76.0 1110 13 US-10-424-599-79603 Sequence 79603, APP  
c 61 15.2 76.0 1287 9 US-09-738-626-2128 Sequence 2128, APP  
c 62 15.2 76.0 1335 13 US-10-476-476-621 Sequence 5276, APP  
c 63 15.2 76.0 1410 13 US-10-627-476-613 Sequence 619, APP  
c 64 15.2 76.0 1513 13 US-10-027-632-253499 Sequence 253499, APP  
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c 68 15.2 76.0 2000 11 US-09-938-842A-4942 Sequence 4942, APP  
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c 72 15.2 76.0 3370 15 US-10-205-823-125 Sequence 02, APP  
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C	136	14.8	74.0	610	16	US-10-027-632-246342	Sequence 246342, A	C	210	14.8	74.0	4564	19	US-10-437-963-45318
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C	143	14.8	74.0	630	13	US-10-027-632-313264	Sequence 313264, A	C	217	14.8	74.0	7741	13	US-10-092-900A-75
C	144	14.8	74.0	640	13	US-10-027-632-89394	Sequence 89394, A	C	218	14.8	74.0	29283	15	US-10-017-161-1987
C	145	14.8	74.0	640	13	US-10-027-632-89395	Sequence 89395, A	C	219	14.8	74.0	29283	16	US-10-292-798-1635
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C	147	14.8	74.0	663	13	US-10-027-632-313264	Sequence 313264, A	C	221	14.8	74.0	33675	9	US-09-921-992-2
C	148	14.8	74.0	663	16	US-10-027-632-313264	Sequence 313264, A	C	222	14.8	74.0	33675	9	US-09-747-810-1
C	149	14.8	74.0	663	16	US-10-027-632-313264	Sequence 313264, A	C	223	14.8	74.0	50426	16	US-10-085-117-160
C	150	14.8	74.0	664	13	US-10-027-632-19342	Sequence 19342, A	C	224	14.8	74.0	50426	16	US-10-085-117-160
C	151	14.8	74.0	665	13	US-10-027-632-279251	Sequence 279251, A	C	225	14.8	74.0	50519	13	US-10-087-192-184
C	152	14.8	74.0	665	16	US-10-027-632-279251	Sequence 279251, A	C	226	14.8	74.0	51052	13	US-10-087-192-184
C	153	14.8	74.0	663	13	US-10-027-632-312220	Sequence 312220, A	C	227	14.8	74.0	51587	17	US-10-322-281-232
C	154	14.8	74.0	663	16	US-10-027-632-312220	Sequence 312220, A	C	228	14.8	74.0	51709	13	US-10-087-192-1198
C	155	14.8	74.0	728	13	US-10-027-632-142284	Sequence 142284, A	C	229	14.8	74.0	51709	14	US-10-003-806-10
C	156	14.8	74.0	728	13	US-10-027-632-142284	Sequence 142284, A	C	230	14.8	74.0	51709	14	US-10-045-120-53
C	157	14.8	74.0	728	16	US-10-027-632-142283	Sequence 142283, A	C	231	14.8	74.0	51709	14	US-10-08

C 234	14.8	74.0	684973	9	US-09-263-959-1	Sequence 1, Appli	c 307	14.2	71.0	171	15	US-10-029-386-27336	Sequence 27336, A
C 235	14.8	74.0	1691139	15	US-10-067-514-1	Sequence 1, Appli	c 308	14.2	71.0	174	13	US-10-085-783A-35599	Sequence 35599, A
C 236	14.8	74.0	1691139	16	US-10-419-723-1	Sequence 44369, A	c 309	14.2	71.0	174	16	US-10-085-783A-35599	Sequence 35599, A
C 237	14.4	72.0	220	13	US-10-424-559-44369	Sequence 10372, A	c 310	14.2	71.0	176	13	US-10-085-783A-17286	Sequence 17286, A
C 238	14.4	72.0	275	17	US-10-437-983-10372	Sequence 99713, A	c 311	14.2	71.0	176	16	US-10-242-535A-17286	Sequence 17286, A
C 239	14.4	72.0	353	13	US-10-427-99-99713	Sequence 4410, AP	c 312	14.2	71.0	190	16	US-10-242-535A-22589	Sequence 22589, A
C 240	14.4	72.0	392	10	US-09-918-995-4410	Sequence 10890, A	c 313	14.2	71.0	209	9	US-09-960-352-8245	Sequence 8245, AP
C 241	14.4	72.0	487	13	US-10-424-559-10890	Sequence 121, APP	c 314	14.2	71.0	218	15	US-10-106-698-1739	Sequence 1739, AP
C 242	14.4	72.0	576	9	US-09-777-564-121	Sequence 30306, A	c 315	14.2	71.0	225	17	US-10-437-963-16904	Sequence 16904, A
C 243	14.4	72.0	576	15	US-10-015-219-121	Sequence 555, APP	c 316	14.2	71.0	227	13	US-10-085-783A-9450	Sequence 9450, AP
C 244	14.4	72.0	582	9	US-09-777-564-555	Sequence 555, APP	c 317	14.2	71.0	227	16	US-10-242-535A-9450	Sequence 9450, AP
C 245	14.4	72.0	582	15	US-10-015-219-555	Sequence 96747, A	c 318	14.2	71.0	234	15	US-10-029-386-14659	Sequence 14659, A
C 246	14.4	72.0	594	13	US-10-027-632-98747	Sequence 30636, A	c 319	14.2	71.0	234	16	US-10-393-840-890	Sequence 890, APP
C 247	14.4	72.0	594	13	US-10-027-632-300306	Sequence 30817, A	c 320	14.2	71.0	247	9	US-09-864-761-20899	Sequence 20899, A
C 248	14.4	72.0	594	16	US-10-027-632-306306	Sequence 30936, A	c 321	14.2	71.0	249	13	US-10-424-599-46366	Sequence 46366, A
C 249	14.4	72.0	594	16	US-10-027-632-308176	Sequence 15825, A	c 322	14.2	71.0	255	10	US-09-930-213-768	Sequence 768, APP
C 250	14.4	72.0	604	17	US-10-027-632-208171	Sequence 20817, A	c 323	14.2	71.0	273	13	US-10-085-783A-13656	Sequence 13656, A
C 251	14.4	72.0	608	13	US-10-027-632-208172	Sequence 20817, A	c 325	14.2	71.0	273	16	US-10-242-535A-13656	Sequence 13656, A
C 252	14.4	72.0	608	13	US-10-027-632-208173	Sequence 20817, A	c 326	14.2	71.0	274	9	US-09-960-352-7665	Sequence 7665, AP
C 253	14.4	72.0	608	16	US-10-027-632-208173	Sequence 20817, A	c 327	14.2	71.0	298	9	US-09-960-352-7665	Sequence 7665, AP
C 254	14.4	72.0	608	16	US-10-027-632-208174	Sequence 20817, A	c 328	14.2	71.0	305	13	US-10-424-599-4051	Sequence 4051, AP
C 255	14.4	72.0	608	13	US-10-027-632-208175	Sequence 20817, A	c 329	14.2	71.0	315	12	US-09-92-293-1129	Sequence 1129, AP
C 256	14.4	72.0	608	16	US-10-027-632-208176	Sequence 20817, A	c 330	14.2	71.0	329	8	US-08-781-986-986	Sequence 13836, A
C 257	14.4	72.0	608	16	US-10-027-632-254270	Sequence 25427, A	c 331	14.2	71.0	329	13	US-10-329-624-986	Sequence 13836, A
C 258	14.4	72.0	608	16	US-10-027-632-254270	Sequence 25427, A	c 332	14.2	71.0	329	9	US-09-764-869-445	Sequence 445, APP
C 259	14.4	72.0	608	16	US-10-027-632-208173	Sequence 20817, A	c 333	14.2	71.0	330	9	US-09-764-869-445	Sequence 445, APP
C 260	14.4	72.0	608	16	US-10-027-632-208173	Sequence 20817, A	c 334	14.2	71.0	330	10	US-09-764-868-182	Sequence 182, APP
C 261	14.4	72.0	608	16	US-10-027-632-217620	Sequence 21762, A	c 335	14.2	71.0	330	13	US-10-424-599-138636	Sequence 13836, A
C 262	14.4	72.0	608	16	US-10-027-632-217620	Sequence 21762, A	c 336	14.2	71.0	330	15	US-10-091-504-445	Sequence 4051, AP
C 263	14.4	72.0	636	13	US-10-027-632-217621	Sequence 21762, A	c 337	14.2	71.0	333	13	US-10-424-599-124672	Sequence 445, APP
C 264	14.4	72.0	636	16	US-10-027-632-254270	Sequence 25427, A	c 338	14.2	71.0	333	15	US-10-029-386-23545	Sequence 2345, A
C 265	14.4	72.0	654	13	US-10-027-632-217620	Sequence 21762, A	c 339	14.2	71.0	341	13	US-10-424-599-11581	Sequence 11581, A
C 266	14.4	72.0	654	13	US-10-027-632-217621	Sequence 21762, A	c 340	14.2	71.0	346	13	US-10-424-599-138636	Sequence 13836, A
C 267	14.4	72.0	654	13	US-10-027-632-217621	Sequence 21762, A	c 341	14.2	71.0	349	13	US-10-424-599-2746	Sequence 2746, APP
C 268	14.4	72.0	654	16	US-10-027-632-217621	Sequence 21762, A	c 342	14.2	71.0	373	13	US-10-027-577-445	Sequence 445, APP
C 269	14.4	72.0	654	16	US-10-027-632-217621	Sequence 21762, A	c 343	14.2	71.0	376	13	US-10-424-599-124672	Sequence 445, APP
C 270	14.4	72.0	654	16	US-10-027-632-217621	Sequence 21762, A	c 350	14.2	71.0	376	13	US-10-424-599-124672	Sequence 445, APP
C 271	14.4	72.0	659	17	US-10-021-952-6838	Sequence 329, APP	c 351	14.2	71.0	376	13	US-10-424-599-124672	Sequence 445, APP
C 272	14.4	72.0	659	13	US-09-810-916-329	Sequence 329, APP	c 352	14.2	71.0	381	13	US-10-028-122A-35860	Sequence 11499, A
C 273	14.4	72.0	659	13	US-09-924-410-329	Sequence 10107, A	c 353	14.2	71.0	382	9	US-09-960-352-11499	Sequence 57310, A
C 274	14.4	72.0	659	13	US-10-424-599-91780	Sequence 20605, A	c 354	14.2	71.0	384	13	US-10-424-535A-28815	Sequence 48729, A
C 275	14.4	72.0	659	17	US-10-451-68-37	Sequence 19245, A	c 355	14.2	71.0	384	13	US-10-424-599-5055	Sequence 48729, A
C 276	14.4	72.0	659	17	US-10-451-68-37	Sequence 19245, A	c 356	14.2	71.0	384	13	US-10-424-599-5055	Sequence 48729, A
C 277	14.4	72.0	672	13	US-10-027-632-252975	Sequence 25295, A	c 357	14.2	71.0	384	16	US-10-424-599-1110	Sequence 1110, APP
C 278	14.4	72.0	672	13	US-10-027-632-252975	Sequence 25295, A	c 358	14.2	71.0	400	13	US-10-085-783A-21844	Sequence 21844, A
C 279	14.4	72.0	672	13	US-10-425-114-20605	Sequence 10248, A	c 359	14.2	71.0	400	16	US-10-242-535A-21844	Sequence 21844, A
C 280	14.4	72.0	672	13	US-10-424-599-91780	Sequence 19245, A	c 360	14.2	71.0	401	9	US-09-864-471-754	Sequence 3921, A
C 281	14.4	72.0	672	13	US-10-424-599-91780	Sequence 19245, A	c 361	14.2	71.0	405	13	US-10-424-599-20669	Sequence 22570, A
C 282	14.4	72.0	672	13	US-10-424-599-91780	Sequence 19245, A	c 362	14.2	71.0	420	13	US-10-424-599-119656	Sequence 36660, A
C 283	14.4	72.0	672	17	US-10-418-972-76	Sequence 25890, A	c 363	14.2	71.0	426	13	US-09-855-783A-35591	Sequence 35591, A
C 284	14.4	72.0	672	17	US-10-418-972-76	Sequence 25890, A	c 364	14.2	71.0	426	16	US-10-242-535A-35591	Sequence 35591, A
C 285	14.4	72.0	672	17	US-10-418-972-76	Sequence 25890, A	c 365	14.2	71.0	430	13	US-10-027-632-73111	Sequence 73111, A
C 286	14.4	72.0	672	17	US-10-418-972-76	Sequence 25890, A	c 366	14.2	71.0	430	16	US-10-027-632-73111	Sequence 73111, A
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C 288	14.4	72.0	672	17	US-10-437-633-8893	Sequence 53078, A	c 368	14.2	71.0	436	13	US-10-027-632-182302	Sequence 5754, AP
C 289	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 369	14.2	71.0	436	16	US-10-027-632-182302	Sequence 5754, AP
C 290	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 370	14.2	71.0	437	16	US-09-918-995-3119	Sequence 31919, A
C 291	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 371	14.2	71.0	442	13	US-10-242-535A-56594	Sequence 56594, A
C 292	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 372	14.2	71.0	442	16	US-10-242-535A-56594	Sequence 56594, A
C 293	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 373	14.2	71.0	450	17	US-10-437-963-33014	Sequence 4421, AP
C 294	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 374	14.2	71.0	457	17	US-10-437-963-33014	Sequence 4421, AP
C 295	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 375	14.2	71.0	460	13	US-09-855-783A-25591	Sequence 26172, A
C 296	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 376	14.2	71.0	460	16	US-10-423-535A-25591	Sequence 26172, A
C 297	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 377	14.2	71.0	466	9	US-09-864-761-385	Sequence 26172, A
C 298	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 378	14.2	71.0	468	13	US-10-085-783A-26172	Sequence 26172, A
C 299	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 379	14.2	71.0	470	9	US-09-988-975-24451	Sequence 26172, A
C 300	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 380	14.2	71.0	470	9	US-09-988-975-24451	Sequence 26172, A
C 301	14.4	72.0	681	17	US-10-418-972-76	Sequence 2651, AP	c 381	14.2	71.0	470	9	US-09-988-975-24451	Sequence 26172, A
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C	382	14.2	71.0	471	9	US-09-864-711-1549	Sequence 10451, A	C 455	14.2	71.0	828	16	US-10-027-632-173549	Sequence 173549,
C	383	14.2	71.0	473	9	US-09-864-711-1549	Sequence 15149, A	C 456	14.2	71.0	842	13	US-10-025-114-21535	Sequence 21535, A
C	384	14.2	71.0	476	13	US-10-027-632-181466	Sequence 181465, A	C 457	14.2	71.0	870	13	US-10-282-1228-27655	Sequence 21655, A
C	385	14.2	71.0	476	16	US-10-027-632-181466	Sequence 181465, A	C 458	14.2	71.0	884	16	US-10-369-493-30485	Sequence 30485, A
C	386	14.2	71.0	476	16	US-10-027-632-181466	Sequence 181465, A	C 459	14.2	71.0	912	13	US-10-424-599-26124	Sequence 26124, A
C	387	14.2	71.0	476	16	US-10-027-632-181466	Sequence 181466, A	C 460	14.2	71.0	915	13	US-10-282-1228-398868	Sequence 398868, A
C	388	14.2	71.0	477	10	US-09-918-995-33549	Sequence 12059, A	C 461	14.2	71.0	928	13	US-10-422-114-19003	Sequence 19003, A
C	389	14.2	71.0	482	10	US-09-918-995-33549	Sequence 33549, A	C 462	14.2	71.0	930	13	US-10-028-1224-27331	Sequence 27331, A
C	390	14.2	71.0	484	9	US-09-864-711-3314	Sequence 3314, A	C 463	14.2	71.0	934	13	US-10-425-114-20130	Sequence 20130, A
C	391	14.2	71.0	486	9	US-09-864-711-5456	Sequence 5456, A	C 464	14.2	71.0	936	13	US-10-422-114-3330	Sequence 3330, A
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C	393	14.2	71.0	506	15	US-10-040-662-2838	Sequence 2838, A	C 466	14.2	71.0	954	13	US-10-425-114-2977	Sequence 2977, A
C	394	14.2	71.0	506	15	US-10-040-662-2838	Sequence 2838, A	C 467	14.2	71.0	970	13	US-10-342-887-2667	Sequence 2667, A
C	395	14.2	71.0	506	16	US-10-154-884B-2838	Sequence 2838, A	C 468	14.2	71.0	970	13	US-10-172-118-2667	Sequence 2667, A
C	396	14.2	71.0	507	15	US-10-029-886-9945	Sequence 9845, A	C 469	14.2	71.0	993	15	US-10-156-761-4079	Sequence 4079, A
C	397	14.2	71.0	521	13	US-10-027-632-312912	Sequence 312912, A	C 470	14.2	71.0	1008	17	US-0-431-963-26292	Sequence 26292, A
C	398	14.2	71.0	521	16	US-10-027-632-312912	Sequence 312912, A	C 471	14.2	71.0	1018	13	US-0-027-632-10345	Sequence 10345, A
C	399	14.2	71.0	534	15	US-10-029-886-13636	Sequence 13636, A	C 472	14.2	71.0	1018	13	US-10-425-114-2977	Sequence 2977, A
C	400	14.2	71.0	548	9	US-09-864-761-6769	Sequence 6769, A	C 473	14.2	71.0	1018	16	US-0-027-632-10346	Sequence 10346, A
C	401	14.2	71.0	548	13	US-10-425-114-16250	Sequence 16250, A	C 474	14.2	71.0	1018	16	US-0-027-632-10346	Sequence 10346, A
C	402	14.2	71.0	548	13	US-10-029-886-850	Sequence 850, A	C 475	14.2	71.0	1025	9	US-09-917-536-25	Sequence 25, A
C	403	14.2	71.0	549	15	US-10-029-886-956	Sequence 956, A	C 476	14.2	71.0	1045	13	US-10-421-114-17568	Sequence 17568, A
C	404	14.2	71.0	554	17	US-10-437-633-33593	Sequence 7353, A	C 477	14.2	71.0	1059	13	US-0-425-114-1667	Sequence 1667, A
C	405	14.2	71.0	558	15	US-10-029-886-2299	Sequence 2299, A	C 478	14.2	71.0	1059	13	US-10-425-114-586	Sequence 586, A
C	406	14.2	71.0	560	15	US-10-029-886-3305	Sequence 3305, A	C 479	14.2	71.0	1060	13	US-10-424-599-35651	Sequence 35651, A
C	407	14.2	71.0	567	13	US-10-240-25-439	Sequence 439, A	C 480	14.2	71.0	1060	13	US-0-027-632-11771	Sequence 11771, A
C	408	14.2	71.0	568	13	US-10-027-632-4922	Sequence 4922, A	C 481	14.2	71.0	1060	13	US-10-027-632-11771	Sequence 11771, A
C	409	14.2	71.0	568	13	US-10-027-632-63505	Sequence 63505, A	C 482	14.2	71.0	1060	13	US-10-027-632-11771	Sequence 11771, A
C	410	14.2	71.0	568	13	US-10-027-632-88501	Sequence 88501, A	C 483	14.2	71.0	1070	13	US-0-425-114-1667	Sequence 1667, A
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C	412	14.2	71.0	568	16	US-10-027-632-63505	Sequence 63505, A	C 485	14.2	71.0	1070	13	US-10-225-0664-991	Sequence 991, A
C	413	14.2	71.0	568	16	US-10-027-632-88501	Sequence 88501, A	C 486	14.2	71.0	1070	13	US-10-374-780A-2813	Sequence 2813, A
C	414	14.2	71.0	569	13	US-10-027-632-24899	Sequence 24899, A	C 487	14.2	71.0	1070	13	US-10-027-632-21035	Sequence 21035, A
C	415	14.2	71.0	569	13	US-10-027-632-24899	Sequence 24899, A	C 488	14.2	71.0	1070	13	US-10-027-632-21035	Sequence 21035, A
C	416	14.2	71.0	589	13	US-10-027-632-24899	Sequence 24899, A	C 489	14.2	71.0	1106	16	US-10-027-632-21035	Sequence 21035, A
C	417	14.2	71.0	589	16	US-10-027-632-24899	Sequence 24899, A	C 490	14.2	71.0	1146	13	US-10-282-12A-20680	Sequence 20680, A
C	418	14.2	71.0	589	16	US-10-027-632-24899	Sequence 24899, A	C 491	14.2	71.0	1148	13	US-10-369-493-32245	Sequence 32245, A
C	419	14.2	71.0	589	16	US-10-027-632-24899	Sequence 24899, A	C 492	14.2	71.0	1148	13	US-10-027-632-212656	Sequence 212656, A
C	420	14.2	71.0	615	17	US-10-437-633-63535	Sequence 63535, A	C 493	14.2	71.0	1156	13	US-10-091-493-52	Sequence 210835, A
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C	422	14.2	71.0	622	13	US-10-027-632-178684	Sequence 178684, A	C 495	14.2	71.0	1176	10	US-0-431-963-49984	Sequence 1444, A
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**RESULT 1**  
 US-09-825-489-3 ; Sequence 3, Application US/09825489  
 ; Publication No. US2003023276A1 ; GENERAL INFORMATION:  
 ; APPLICANT: AGRAWAL, SUDHIR  
 ; APPLICANT: KANDIMALA, EKUMBAR R.  
 ; APPLICANT: BREGMAN, DAVID B.  
 ; APPLICANT: MANTI, SRIDHAR  
 ; TITLE OF INVENTION: SENSITIZATION OF CELLS TO CYTOTOXIC AGENTS USING OLIGONUCLEOTIDES DIRECTED TO NUCLEOTIDE EXCISION REPAIR

**ALIGNMENTS**

; TITLE OF INVENTION: OR TRANSCRIPTION COUPLED REPAIR GENES  
 ; FILE REFERENCE: HY2-075US2 (475,08,514)  
 ; CURRENT APPLICATION NUMBER: US/09/825,489  
 ; CURRENT FILING DATE: 2001-04-03  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: oligonucleotide  
 ; OTHER INFORMATION: US-09-825-489-3  
  
 Query Match 100.0%; Score 20; DB 11; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGTCATACATCATGTGATG 20  
 Db 1 GGTCATACATCATGTGATG 20  
  
 RESULT 2  
 US-09-867-701-7544  
 ; Sequence 7544, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121-497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 7544  
 ; LENGTH: 486  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(486)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-867-701-7544  
  
 Query Match 100.0%; Score 20; DB 9; Length 486;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGTCATACATCATGTGATG 20  
 Db 149 GGTCATACATCATGTGATG 168  
  
 RESULT 3  
 US-09-867-701-2117/c  
 ; Sequence 2117, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121-497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 13  
 ; LENGTH: 1377  
  
 RESULT 4  
 US-09-867-701-2107  
 ; Sequence 2107, Application US/09867701  
 ; Patent No. US20020132237A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aglate, Paul A.  
 ; APPLICANT: Jones, Robert  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
 ; FILE REFERENCE: 210121-497  
 ; CURRENT APPLICATION NUMBER: US/09/867,701  
 ; CURRENT FILING DATE: 2001-05-29  
 ; NUMBER OF SEQ ID NOS: 10912  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 2107  
 ; LENGTH: 513  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(513)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-867-701-2107  
  
 Query Match 100.0%; Score 20; DB 9; Length 513;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGTCATACATCATGTGATG 20  
 Db 357 GGTCATACATCATGTGATG 376  
  
 RESULT 5  
 US-09-825-489-13/c  
 ; Sequence 13, Application US/09825489  
 ; Publication No. US20030232767A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AGRAWAL, SUDHIR  
 ; APPLICANT: KANDIMALLA, EKAMBAR R.  
 ; APPLICANT: BREGMAN, DAVID B.  
 ; APPLICANT: MANTI, SRIDHAR  
 ; APPLICANT: LU, YI  
 ; TITLE OF INVENTION: SENSITIZATION OF CELLS TO CYTOTOXIC AGENTS USING  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES DIRECTED TO NUCLEOTIDE EXCISION REPAIR  
 ; FILE REFERENCE: HY2-075US2 (475,08,514)  
 ; CURRENT APPLICATION NUMBER: US/09/825,489  
 ; CURRENT FILING DATE: 2001-04-03  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 13  
 ; LENGTH: 1377

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-825-489-13

Query Match 100.0%; Score 20; DB 11; Length 1377;
Best Local Similarity 100.0%; Pred. No. 5.3%; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
US-10-103-313-116/c
; Sequence 116, Application US/10103313
; Publication No. US20030082758A1

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P207C1
; CURRENT APPLICATION NUMBER: US/10/103,313
; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 653

; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 116
; LENGTH: 1407
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-103-313-116

Query Match 100.0%; Score 20; DB 15; Length 1407;
Best Local Similarity 100.0%; Pred. No. 5.3%; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-10-101-510-587
; Sequence S87, Application US/10101510
; Publication No. US20030148295A1

; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 1517-0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 587
; LENGTH: 4670
; TYPE: DNA
; ORGANISM: Homo sapiens

; FEATURE: NAME/KEY: modified_base
; LOCATION: (1781)..(17894)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE: NAME/KEY: modified_base
; LOCATION: (2658)..(3015)
; OTHER INFORMATION: a, t, c, g, other or unknown

Query Match 100.0%; Score 20; DB 15; Length 4670;
Best Local Similarity 100.0%; Pred. No. 6.6%; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-10-027-632-257254/c
; Sequence 257254, Application US/10027632
; Publication No. US20020198371A1

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 32520
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 257254
; LENGTH: 1526
; TYPE: DNA
; ORGANISM: Human

US-10-027-632-257254

Query Match 85.0%; Score 17; DB 13; Length 1526;
Best Local Similarity 100.0%; Pred. No. 1.8e+02%; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-10-027-632-257254/c
; Sequence 257254, Application US/10027632
; Publication No. US20020204075A9

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09

```



Qy 3 TCCATACTCATCTTGATG 20  
Db ||||| | | | | | | | | | | | | | |  
 Qy 71 TCCATTCTCAAGTGTGAC 54  
 ;  
 RESULT 13  
 US-10-085-783A-40734  
 ; Sequence 40734, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; APPLICANT: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/1-002  
 ; CURRENT APPLICATION NUMBER: US/10/085, 783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/1305, 340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275, 017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271, 955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 40734  
 ; LENGTH: 238  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-242-535A-40734  
 Query Match 79.0%; Score 15.8; DB 13; Length 238;  
 Best Local Similarity 89.5%; Pred. No. 5.2e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 2;  
 Qy 2 GTCCATACTCATGTGTGATG 20  
 Db 77 GTCCATATACTCAAGTGTGAC 95  
 ;  
 RESULT 14  
 US-10-242-535A-40734  
 ; Sequence 40734, Application US/10242535A  
 ; Publication No. US20040013663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; APPLICANT: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/1-005  
 ; CURRENT APPLICATION NUMBER: US/10/242, 535A  
 ; PRIOR FILING DATE: 2002-09-12  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/1305, 340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275, 017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271, 955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 40734  
 ; LENGTH: 238  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-242-535A-40734  
 Query Match 79.0%; Score 15.8; DB 16; Length 239;  
 Best Local Similarity 89.5%; Pred. No. 5.2e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 2;  
 Qy 2 GTCCATACTCATGTGTGATG 20  
 Db 77 GTCCATATACTCAAGTGTGAC 95  
 ;  
 RESULT 15  
 US-09-732-627A-2949/c  
 ; Sequence 2949, Application US/09732627A  
 ; Publication No. US20040123338A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fincher, Karen L.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; FILE REFERENCE: 38-2-(51770)B  
 ; CURRENT APPLICATION NUMBER: US/09/732, 627A  
 ; CURRENT FILING DATE: 2000-12-08  
 ; NUMBER OF SEQ ID NOS: 4930  
 ; SEQ ID NO 2949  
 ; LENGTH: 296  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3493-010-P1-M1-E9  
 ; US-09-732-627A-2949  
 Query Match 79.0%; Score 15.8; DB 12; Length 296;  
 Best Local Similarity 89.5%; Pred. No. 5.4e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 2;  
 Qy 2 GTCCATACTCATGTGTGATG 20  
 Db 29 GTCCATATACTCAAGTGTGAC 11  
 ;  
 RESULT 16  
 US-10-060-036-3118/c  
 ; Sequence 3118, Application US/10060036  
 ; Publication No. US20030073144A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Benson, Darin R.  
 ; APPLICANT: Kalob, Michael D.  
 ; APPLICANT: Lodes, Michael J.  
 ; APPLICANT: Persing, David H.  
 ; APPLICANT: Hepler, William T.  
 ; APPLICANT: Jiang, Yuqiu  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
 ; FILE REFERENCE: 210121.566  
 ; CURRENT APPLICATION NUMBER: US/10/060, 036  
 ; CURRENT FILING DATE: 2002-01-30  
 ; NUMBER OF SEQ ID NOS: 4560  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 3118  
 ; LENGTH: 431  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: III, 284  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-10-060-036-3118  
 Query Match 79.0%; Score 15.8; DB 15; Length 431;  
 Best Local Similarity 89.5%; Pred. No. 5.8e+02; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 2;  
 Qy 2 GTCCATACTCATGTGTGATG 20  
 Db 194 GTCCATATACTCAAGTGTGAC 176  
 ;  
 RESULT 17  
 US-09-918-995-12216/c  
 ; Sequence 12216, Application US/09918995  
 ; Publication No. US20030073623A1

GENERAL INFORMATION:  
 APPLICANT: Ifyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FROM VARIOUS cDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/918,995  
 PRIOR FILING DATE: 2001-07-30  
 PRIOR FILING DATE: 2001-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 12216  
 LENGTH: 462  
 TYPE: DNA  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(462)  
 OTHER INFORMATION: n = A,T,C or G  
 ; US-09-918-995-12216

Query Match 79.0%; Score 15.8; DB 10; Length 462;  
 Best Local Similarity 89.5%; Pred. No. 5.9e+02;  
 Matches 17; Conservative 0; Mismatches 2;  
 Qy 2 GTCCATACTCATGTGATG 20  
 Db 446 GTCCCTCTCAAGTGTGAT 428

RESULT 18  
 US-10-085-783A-45577/c  
 ; Sequence 45577, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; APPLICANT: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; CURRENT APPLICATION NUMBER: US 60/3105,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 45577  
 ; LENGTH: 540  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-085-783A-45577

Query Match 79.0%; Score 15.8; DB 13; Length 540;  
 Best Local Similarity 89.5%; Pred. No. 5.1e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GTCCTCATACTATGTGAT 19  
 Db 233 GTCACACAAATCATGTGAT 215

RESULT 19  
 US-10-242-535A-45577/c  
 ; Sequence 45577, Application US/10242535A  
 ; Publication No. US20040013663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; APPLICANT: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242,535A  
 CURRENT FILING DATE: 2002-09-12  
 PRIOR APPLICATION NUMBER: US 10/085,783  
 PRIOR FILING DATE: 2002-02-28  
 PRIOR APPLICATION NUMBER: US 60/305,340  
 PRIOR FILING DATE: 2001-07-13  
 PRIOR APPLICATION NUMBER: US 60/275,017  
 PRIOR FILING DATE: 2001-01-12  
 PRIOR APPLICATION NUMBER: US 60/271,955  
 PRIOR FILING DATE: 2001-02-28  
 NUMBER OF SEQ ID NOS: 58994  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 45577  
 LENGTH: 540  
 TYPE: DNA  
 ORGANISM: Human  
 ; US-10-242-535A-45577

Query Match 79.0%; Score 15.8; DB 16; Length 540;  
 Best Local Similarity 89.5%; Pred. No. 6.1e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GGTCCATACTCATGTGAT 19  
 Db 233 GGTCCACAAATCATGTGAT 215

RESULT 20  
 US-09-871-161-62  
 ; Sequence 62, Application US/09871161  
 ; Publication No. US20030097666A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ENDEGE, WILSON O., ET AL.  
 ; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION  
 ; FILE REFERENCE: CCNA-260X  
 ; CURRENT APPLICATION NUMBER: US/09/871,161  
 ; CURRENT FILING DATE: 2001-05-31  
 ; PRIOR APPLICATION NUMBER: 09/328,111  
 ; PRIOR FILING DATE: 1999-05-08  
 ; PRIOR APPLICATION NUMBER: 60/117,393  
 ; PRIOR FILING DATE: 1999-01-27  
 ; PRIOR APPLICATION NUMBER: 60/098,639  
 ; PRIOR FILING DATE: 1998-09-31  
 ; NUMBER OF SEQ ID NOS: 544  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 62  
 ; LENGTH: 614  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(614)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-871-161-62

Query Match 79.0%; Score 15.8; DB 10; Length 614;  
 Best Local Similarity 89.5%; Pred. No. 6.2e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 GTCCATACTCATGTGATG 20  
 Db 466 GTCCATAATCAGTGTGAT 484

RESULT 21  
 US-10-641-643-1225/c  
 ; Sequence 1225, Application US/0641643  
 ; Publication No. US20040077003A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Coccia, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
GENE EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/641,643

FILING DATE: 14-Aug-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1225:

SEQUENCE CHARACTERISTICS:

LENGTH: 68 base Pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: Linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g246741

SEQUENCE DESCRIPTION: SEQ ID NO: 1225 :

US-10-641-643-1225

Query Match 79.0%; Score 15.8; DB 17; Length 686;  
Best Local Similarity 89.5%; Pred. No. 6.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCATACTCATGTGAT 19

Db 628 GGTCATACTCATGTGAT 610

RESULT 22

US-10-424-599-20394

; Sequence 20394, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J.

; APPLICANT: Kovacic David K.

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 20394

; LENGTH: 765

; TYPE: DNA

; FEATURE: ORGANISM: Glycine max

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_118420C.1

; US-10-424-599-20394

RESULT 23

US-10-437-963-64475

; Sequence 64475, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: Li, Ping

; APPLICANT: Barabuk, Brad

; APPLICANT: Zhou, Yihua

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Kovacic, David K.

; APPLICANT: Cao, Yongwei

; APPLICANT: Zhou, Yihua

; APPLICANT: Wu, Wei

; APPLICANT: Barabuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 7531

; LENGTH: 1329

; TYPE: DNA

; FEATURE: ORGANISM: Oryza sativa

; OTHER INFORMATION:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_14117C.1  
; US-10-437-963-7531

Query Match 79.0%; Score 15.8; DB 17; Length 1329;  
Best Local Similarity 89.5%; Pred. No. 9.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCCATACTCATGTGATG 20  
Db 355 GTCCATCTCATGTGATG 373

RESULT 25  
US-10-041-018-111  
; Sequence 111; Application US/10041018  
; Publication No. US20040072323A1  
; GENERAL INFORMATION:  
; APPLICANT: Matsuda, Seiichi P.T.  
; APPLICANT: Hart, Elizabeth A.  
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism  
; FILE REFERENCE: P0208011/0025647  
; CURRENT APPLICATION NUMBER: US/10/041,018  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: US 60/259880  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 111  
; LENGTH: 3021  
; TYPE: DNA  
; ORGANISM: *Dendroctonus jeffreyi*  
; US-10-041-018-111

Query Match 79.0%; Score 15.8; DB 12; Length 3021;  
Best Local Similarity 89.5%; Pred. No. 3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCCATACTCATGTGATG 20  
Db 2142 GTCCATGCTCTGTGATG 2160

RESULT 26  
US-10-041-018-112  
; Sequence 112; Application US/10041018  
; Publication No. US20040072323A1  
; GENERAL INFORMATION:  
; APPLICANT: Matsuda, Seiichi P.T.  
; APPLICANT: Hart, Elizabeth A.  
; TITLE OF INVENTION: Diterpene-Producing Unicellular Organism  
; FILE REFERENCE: P0208011/0025647  
; CURRENT APPLICATION NUMBER: US/10/041,018  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: US 60/259880  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 413  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 112  
; LENGTH: 5874  
; TYPE: DNA  
; ORGANISM: *Dendroctonus jeffreyi*  
; US-10-041-018-112

Query Match 79.0%; Score 15.8; DB 12; Length 5874;  
Best Local Similarity 89.5%; Pred. No. 9.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCCATACTCATGTGATG 20  
Db 4943 GTCCATGCTCTGTGATG 4961

RESULT 27  
US-10-027-632-79848  
; Sequence 632; Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827-129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/1218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-03-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-03-09  
; NUMBER OF SEQ ID NOS: 32520  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 79848  
; LENGTH: 519  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-027-632-79848

Query Match 77.0%; Score 15.4; DB 13; Length 519;  
Best Local Similarity 94.1%; Pred. No. 9.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCATACATCATGTTGATG 20 ; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 79848  
; LENGTH: 519;  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-027-632-79848

RESULT 29  
; Sequence 79849, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827-129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; APPLICATION NUMBER: US 60/198,676  
; PRIORITY FILING DATE: 2000-04-20 ; Publication No. US20030204075A9  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; APPLICATION NUMBER: US 60/167,363  
; PRIORITY FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 79849  
; LENGTH: 519  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-027-632-79849

RESULT 30  
; Sequence 79848, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827-129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIORITY FILING DATE: 1999-09-28  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 79849  
; LENGTH: 519  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-027-632-79849

RESULT 31  
; Sequence 79849, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827-129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIORITY FILING DATE: 1999-09-28  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 79849  
; LENGTH: 519  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-027-632-79849

RESULT 32  
; Sequence 497, Application US/03764847  
; Publication No. US20020132767A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PCT009  
; CURRENT APPLICATION NUMBER: US/09/764,847  
; CURRENT FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SEQ ID NO: 497  
; LENGTH: 551

TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: SITE  
 NAME/KEY: SITE  
 LOCATION: (398)  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: SITE  
 LOCATION: (477)  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: SITE  
 LOCATION: (479)  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: SITE  
 LOCATION: (532)  
 OTHER INFORMATION: n equals a, t, g, or c  
 US-09-761-847-497  
 Query Match 77.0%; Score 15.4; DB 9; Length 551;  
 Best Local Similarity 94.1%; Pred. No. 9.7e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TCCATCATCTAGTGTAT 19  
 Db 261 TCCATTCTCATGTTAT 277

RESULT 33  
 US-10-093-154-497  
 Sequence 497, Application US/10092154  
 Publication No. US20030054375A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: PC005C1  
 CURRENT APPLICATION NUMBER: US/10/092,154  
 CURRENT FILING DATE: 2002-03-07  
 NUMBER OF SEQ ID NOS: 2003  
 prior Application removed - See File Wrapper or Palm  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 497  
 LENGTH: 551  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE: SITE  
 NAME/KEY: misc\_feature  
 LOCATION: (398)  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: misc\_feature  
 LOCATION: (477)  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: misc\_feature  
 LOCATION: (478)  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: misc\_feature  
 LOCATION: (479)  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: misc\_feature  
 LOCATION: (532)  
 OTHER INFORMATION: n equals a, t, g, or c  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: misc\_feature  
 LOCATION: (479)  
 OTHER INFORMATION: n equals a, t, g, or c  
 NAME/KEY: misc\_feature  
 LOCATION: (532)  
 OTHER INFORMATION: n equals a, t, g, or c  
 OTHER INFORMATION: n equals a, t, g, or c  
 US-10-093-154-497  
 Query Match 77.0%; Score 15.4; DB 9; Length 551;  
 Best Local Similarity 94.1%; Pred. No. 9.7e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TCCATCATCTAGTGTAT 19  
 Db 261 TCCATTCTCATGTTAT 277

RESULT 34  
 US-10-027-632-66707/C  
 Sequence 66707, Application US/10027632  
 Publication No. US20020198371A1  
 GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827-129  
 CURRENT APPLICATION NUMBER: US/10/027,632  
 CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483  
 PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/185,218  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483  
 PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/185,218  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SEQ ID NO 66707  
 LENGTH: 573  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-027-632-66707  
 Sequence 66708, Application US/10027632  
 Publication No. US20020198371A1  
 GENERAL INFORMATION:  
 APPLICANT: Wang, David G.  
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
 FILE REFERENCE: 108827-129  
 CURRENT APPLICATION NUMBER: US/10/027,632  
 CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006  
 PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483  
 PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/185,218  
 PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/198,676  
 PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358  
 PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002  
 PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720  
 SEQ ID NO 66708  
 LENGTH: 573  
 TYPE: DNA  
 ORGANISM: Human

US-10-027-632-66708

Query Match 77.0%; Score 15.4; DB 13; Length 573;  
 Best Local Similarity 94.1%; Pred. No. 9.8e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATACTCACTGTTAAT 19  
 Db 471 TCCATACTCACTGTTAAT 455

RESULT 36

US-10-027-632-311196/c  
 Sequence 311196, Application US/10027632

; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 FILE REFERENCE: 108827.129  
 CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 311196  
 LENGTH: 573

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-311196

Query Match 77.0%; Score 15.4; DB 13; Length 573;  
 Best Local Similarity 94.1%; Pred. No. 9.8e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATACTCACTGTTAAT 19  
 Db 471 TCCATACTCACTGTTAAT 455

RESULT 37

US-10-027-632-311197/c  
 Sequence 311197, Application US/10027632

; Publication No. US20020198371A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 FILE REFERENCE: 108827.129  
 CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 66707  
 LENGTH: 573

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-66707

Query Match 77.0%; Score 15.4; DB 16; Length 573;  
 Best Local Similarity 94.1%; Pred. No. 9.8e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATACTCACTGTTAAT 19  
 Db 471 TCCATACTCACTGTTAAT 455

RESULT 38

US-10-027-632-66707/c  
 Sequence 66707, Application US/10027632

; Publication No. US20030204075A9  
 ; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 FILE REFERENCE: 108827.129  
 CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30  
 PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12  
 PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23  
 PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28  
 PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09  
 NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 66707  
 LENGTH: 573

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-66707

Query Match 77.0%; Score 15.4; DB 16; Length 573;  
 Best Local Similarity 94.1%; Pred. No. 9.8e+02;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATACTCACTGTTAAT 19  
 Db 471 TCCATACTCACTGTTAAT 455

RESULT 39

US-10-027-632-66708/c  
 Sequence 66708, Application US/10027632

; Publication No. US20030204075A9  
 ; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 FILE REFERENCE: 108827.129  
 CURRENT APPLICATION NUMBER: US 60/198,676

CURRENT FILING DATE: 2000-04-30  
 PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218  
 PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363  
 PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29  
 PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-01-12  
 PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20  
 PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-02-24  
 PRIOR APPLICATION NUMBER: US 60/167,363

SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 311197  
 LENGTH: 573

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-66708

CURRENT APPLICATION NUMBER: US/10/0227,632  
; CURRENT APPLICATION NUMBER: US/10/0227,632  
; PRIORITY FILING DATE: 2002-04-30  
; PRIORITY APPLICATION NUMBER: US 60/218,006  
; PRIORITY FILING DATE: 2000-07-12 ; Sequence 311197, Application US/10027632  
; PRIORITY APPLICATION NUMBER: US 60/198,676 ; Publication No. US2003024075A9  
; PRIORITY APPLICATION NUMBER: US 60/193,483 ; GENERAL INFORMATION:  
; PRIORITY FILING DATE: 2000-03-29 ; APPLICANT: Wang, David G.  
; PRIORITY APPLICATION NUMBER: US 60/185,218 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; PRIORITY FILING DATE: 2000-02-24 ; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; PRIORITY APPLICATION NUMBER: US 60/167,363 ; FILE REFERENCE: 108827-129  
; PRIORITY FILING DATE: 1999-11-23 ; CURRENT APPLICATION NUMBER: US/10/027,632  
; PRIORITY APPLICATION NUMBER: US 60/156,358 ; CURRENT FILING DATE: 2002-04-30  
; PRIORITY FILING DATE: 1999-09-28 ; PRIORITY APPLICATION NUMBER: US/10/027,632  
; PRIORITY APPLICATION NUMBER: US 60/146,002 ; PRIORITY FILING DATE: 2000-02-24  
; PRIORITY FILING DATE: 1999-08-09 ; PRIORITY APPLICATION NUMBER: US 60/167,363  
; NUMBER OF SEQ ID NOS: 325720 ; PRIORITY FILING DATE: 2000-04-20  
; SOFTWARE: Fast-SEQ for Windows Version 4.0 ; PRIORITY APPLICATION NUMBER: US 60/193,483  
; SEQ ID NO 66708 ; PRIORITY FILING DATE: 2000-03-29  
; LENGTH: 573 ; PRIORITY APPLICATION NUMBER: US 60/185,218  
; TYPE: DNA ; PRIORITY FILING DATE: 2000-07-12  
; ORGANISM: Human ; PRIORITY APPLICATION NUMBER: US 60/198,676  
; ; US-10-027-632-66708  
Query Match 77.0%; Score 15.4; DB 16; Length 573;  
Best Local Similarity 94.1%; Pred. No. 9.8e+02; Mismatches 1;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 TCCATACATCATGTGAT 19  
Db 471 TCCATACATCATGTGAT 455  
; RESULT 40  
; US-10-027-632-311196/c  
; Sequence 311196, Application US/10027632  
; Publication No. US2003024075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827-129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIORITY APPLICATION NUMBER: US 60/218,006  
; PRIORITY FILING DATE: 2000-07-12  
; PRIORITY APPLICATION NUMBER: US 60/198,676  
; PRIORITY FILING DATE: 2000-04-20  
; PRIORITY APPLICATION NUMBER: US 60/193,483  
; PRIORITY FILING DATE: 2000-03-29  
; PRIORITY APPLICATION NUMBER: US 60/185,218  
; PRIORITY FILING DATE: 2000-02-24  
; PRIORITY APPLICATION NUMBER: US 60/167,363  
; PRIORITY FILING DATE: 1999-11-23  
; PRIORITY APPLICATION NUMBER: US 60/156,358  
; PRIORITY FILING DATE: 1999-09-28  
; PRIORITY APPLICATION NUMBER: US 60/146,002  
; PRIORITY FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 311197  
; LENGTH: 573  
; TYPE: DNA  
; ORGANISM: Human  
; ; US-10-027-632-311197  
; US-10-027-632-311197  
Query Match 77.0%; Score 15.4; DB 16; Length 573;  
Best Local Similarity 94.1%; Pred. No. 9.8e+02; Mismatches 1;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 TCCATACATCATGTGAT 19  
Db 471 TCCATACATCATGTGAT 455  
; RESULT 42  
; US-10-424-599-103050  
; Sequence 103050, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; APPLICANT: Zhou Yihua  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(52223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 103050  
; LENGTH: 715  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE: OTHER INFORMATION: Clone ID: PAT\_MRT3847\_54071C.1  
; ; US-10-424-599-103050  
Query Match 77.0%; Score 15.4; DB 13; Length 715;  
Best Local Similarity 94.1%; Pred. No. 1e+03; Mismatches 1;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 TCCATACATCATGTGAT 19  
Db 471 TCCATACATCATGTGAT 455

Db 368 CCATGCTCATGTGATG 384 US-09-754-853A-2/c  
; Sequence 2, Application US/09754853A  
; Publication No. US20030005491A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauge, Brian M.  
; APPLICANT: Hauge, Laurence D.  
; APPLICANT: Parsons, Jeremy D.  
; APPLICANT: Wang, Ming Li.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With FILE REFERENCE: 38-10115810B  
; TITLE OF INVENTION: Soybean Cyst Nematode Resistance  
; FILE REFERENCE: 38-10115810B  
; CURRENT APPLICATION NUMBER: US/09754, 853A  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174, 880  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 1119  
; SEQ ID NO 2 LENGTH: 335913  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_121097C.1  
US-10-424-599-23361 US-09-754-853A-2  
; Sequence 3, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhardt, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR FILE REFERENCE: 52945200122  
; CURRENT APPLICATION NUMBER: US/10/087, 192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747, 377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798, 586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 1807 LENGTH: 119414  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(119414)  
; OTHER INFORMATION: n = A, T, C or G ;  
US-10-087-192-1807 LENGTH: 119414  
; Query Match Best Local Similarity 97.0%; Score 15.4; DB 13; Length 119414; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
; SEQ ID NO 2 GTCCATACTCTGTGA 18 LENGTH: 335913  
; Query Match Best Local Similarity 94.1%; Score 15.4; DB 10; Length 335913; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
; Db 11805 GTCCATACATCTATGTGA 11789 LENGTH: 335913  
; Query Match Best Local Similarity 94.1%; Score 15.4; DB 10; Length 335913; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
; Db 24565 TCCAAGTCATGTGAT 24549 LENGTH: 335913  
; Query Match Best Local Similarity 94.1%; Score 15.4; DB 10; Length 335913; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
; OTHER INFORMATION: Clone ID: 240017\_region\_G3  
US-09-754-853A-3 LENGTH: 335913  
; Sequence 3, Application US/09754853A  
; Publication No. US20030005491A1  
; GENERAL INFORMATION:  
; APPLICANT: Hauge, Brian M.  
; APPLICANT: Parnell, Laurence D.  
; APPLICANT: Parsons, Jeremy D.  
; APPLICANT: Wang, Ming Li.  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With FILE REFERENCE: 38-10115810B  
; CURRENT APPLICATION NUMBER: US/09754, 853A  
; CURRENT FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 60/174, 880  
; PRIOR FILING DATE: 2000-01-07  
; NUMBER OF SEQ ID NOS: 1119  
; SEQ ID NO 3 LENGTH: 335913  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (46798)..(48973), (49975)..(49573)  
; OTHER INFORMATION: Clone ID: 240017\_region\_G3  
US-09-754-853A-3 LENGTH: 335913  
; Query Match Best Local Similarity 97.0%; Score 15.4; DB 10; Length 335913; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
; Query Match Best Local Similarity 94.1%; Score 15.4; DB 10; Length 335913; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Sequence 127062, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovacic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5322)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285694  
; SEQ ID NO: 127062  
; LENGTH: 292  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PRM\_MRM13847\_85743C.1  
; US-10-424-599-127062

Query Match 76.0%; Score 15.2; DB 13; Length 292;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GGTCCATACTCATGTGATG 20  
Db 284 GGACCAACTCATGTGATG 303

RESULT 48  
US-08-781-986A-1137  
; Sequence 1137, Application US/08781986A  
; Publication No. US2003005436A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunisch  
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 5255  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/329,624  
; FILING DATE: 27-Dec-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/956,171  
; FILING DATE: October 20, 1997  
; APPLICATION NUMBER: 60/009,861  
; FILING DATE: January 5, 1996  
; APPLICATION NUMBER: 08/781,986  
; FILING DATE: January 3, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mark J. Hyman  
; REGISTRATION NUMBER: 46,789  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (240) 314-1224  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 1137:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 330 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1137:  
; US-10-329-624-1137

Query Match 76.0%; Score 15.2; DB 13; Length 330;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GGTCCATACTCATGTGATG 20  
Db 284 GGACCAACTCATGTGATG 303

RESULT 50  
US-10-424-599-130364  
; Sequence 130364, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J  
APPLICANT: Kovacic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 28564  
SEQ ID NO 130364  
LENGTH: 358  
TYPE: DNA  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_88727C.1  
US-10-424-599-130364

Query Match 76.0%; Score 15.2; DB 13; Length 358;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GGTCCATACTCTGTGATG 20  
Db 97 GGCTCTATAATCTGTGATG 116

Search completed: August 17, 2004, 16:56:43  
Job time : 396 SECs

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: August 17, 2004, 13:20:27 ; Search time 1548 Seconds  
 Perfect score: 20 US-09-825-489-3  
 Sequence: 1 ggtccatatactcatgttgatg 20

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqB, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 800 summaries

Database : GenEmbl:

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pi:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_on:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_p1:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_btg\_hum:\*

31: em\_btg\_inv:\*

32: em\_btg\_other:\*

33: em\_btg\_mus:\*

34: em\_btg\_p1n:\*

35: em\_btg\_rod:\*

36: em\_btg\_man:\*

37: em\_btg\_vrt:\*

38: em\_sy:\*

39: em\_btg\_hum:\*

40: em\_btg\_mus:\*

41: em\_btg\_other:\*

Pred. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match Length	DB	ID	Description
1	20	100	0	20	AX282880 Sequence
2	20	100	0	809	HSXPAC5 U10347 Human Xerod AR183106
3	20	100	0	822	AR183106 Sequence AR203243
4	20	100	0	822	AX277000 Sequence AX277000
5	20	100	0	822	AX277000 Sequence AX277000
6	20	100	0	1377	6 AX282890 Sequence D14533 Homo sapien BC019495 Homo sapien BC019495 Homo sapien
7	20	100	0	1439	9 BC019495 ARF503166 Homo sapien ARF03166 Homo sapien ARF03166 Homo sapien
8	20	100	0	24994	9 ARF503166 Homo sapien ARF45531 Human DNA AL442130 Homo sapi
9	20	100	0	11345	9 ARF45531 Human DNA AL442130 Homo sapi
10	20	100	0	167079	2 AL442130 Homo sapi
11	20	100	0	167079	2 AL442130 Homo sapi
12	18.4	92.0	1095	5 XBLXPACB2 D31895 Xenopus lae	
13	18.4	92.0	1277	6 XBLXPACB2 D31895 Xenopus lae	
14	18.4	92.0	157653	10 AL732555 Mouse DNA AL732555 Mouse DNA	
15	18.4	92.0	19263	2 AC108694 Rattus no AC108694 Rattus no	
16	18.4	92.0	19263	2 AC126124 AC126124 Rattus no	
17	17.4	87.0	158826	8 AP003607 AP003607 Oryza sat	
18	17.4	87.0	197674	2 AP004367 AP004367 Oryza sat	
19	17.4	87.0	198448	10 AC15118 Mus muscu AC004682 Homo sapi	
20	17	82.0	199134	9 HUAC004682 AC004682 Homo sapi	
21	17	85.0	190856	2 AC009160 AC009160 Homo sapi	
22	17	85.0	203297	2 AC134076 AC134076 Rattus no	
23	17	85.0	203730	2 AC094314 AC094314 Oryza sat	
24	16.8	84.0	294	10 MMXPAC6 AP003367 Oryza sat	
25	16.8	84.0	576	10 AF354052 Mus muscu	
26	16.8	84.0	938	10 MMXPAC7 X71351 M_musculus AX568974 Sequence	
27	16.8	84.0	1029	16 AX566974 Continuation [2 of BX537312 Danio rer	
28	16.8	84.0	2138	3 AX115474 Ciona int AE007333 Streptoco	
29	16.8	84.0	11344	1 AP07333 AP07333 Rattus no	
30	16.8	84.0	14273	6 AR218808 Sequence	
31	16.8	84.0	14273	6 BD0031720 Polynucleotide	
32	16.8	84.0	90169	9 HUAC004682 Homo sapi	
33	16.8	84.0	1029	2 AC0095009_1 AC011144 Homo sapi	
34	16.8	84.0	110000	2 AC0095009_1 AC011144 Homo sapi	
35	16.8	84.0	121113	2 AC15474 Ciona int AE007333 Streptoco	
36	16.8	84.0	127247	9 HS326113 Z82170 Human DNA	
37	16.8	84.0	129300	8 AP003886 Oryza sat	
38	16.8	84.0	148416	9 AC002089 AC002089 Homo sapi	
39	16.8	84.0	152635	10 AC011144 Homo sapi	
40	16.8	84.0	155646	9 AC146044 Pan trogl	
41	16.8	84.0	157200	9 AP005233 Homo sapi	
42	16.8	84.0	164572	8 OSJUN00128 AL601001 Oryza sat	
43	16.8	84.0	175936	2 SPNEU1908 AL449930 Streptoco	
44	16.8	84.0	180388	2 AC139894 Rattus no	
45	16.8	84.0	181984	2 AC139894 Rattus no	
46	16.8	84.0	209706	2 AC119611 Homo sapi	
47	16.8	84.0	213381	10 AC129598 Pan trogl	
48	16.8	84.0	216911	10 AC107756 Homo sapi	
49	16.8	84.0	235182	2 AC107742 Oryza sat	
50	16.8	84.0	30340	1 AB016936 Bacteroid	
51	16.8	84.0	349980	6 AX517160 AX517160 Sequence	
52	16.8	84.0	3573	1 DLJ000883 AJ000883 Lactococc	
53	16.4	82.0	6765	6 AX586945 Sequence	
54	16.4	82.0	7568	1 ARF092042 Lactococc	
55	16.4	82.0	10240	1 AB005382 Bacteroid	
56	16.4	82.0	15246	6 AX586923 Sequence	
57	16.4	82.0	22868	9 AF536318 AF536318 Homo sapi	
58	16.4	82.0	49321	10 AF275364S3 AF275364S3 Homo sapi	
59	16.4	82.0	7568	1 ARF092042 Lactococc	
60	16.4	82.0	92487	9 AC058280 Homo sapi	
61	16.4	82.0	15246	6 AC105432 Magnapor	
62	16.4	82.0	93388	9 AL390240 Human DNA	
63	16.4	82.0	10000	2 AC11405_1 Continuation [2 of	
64	16.4	82.0	15768	2 AP000712 Homo sapi	
65	16.4	82.0	137411	2 AC124678 Mus muscu	

C	66	16.4	82.0	137569	2	AC094093	Homo sapi	c	139	15.8	79.0	1804	10	MMS76SIAD
C	67	16.4	82.0	140730	9	AK001960	Homo sapi	c	140	15.8	79.0	1844	8	AK103896
C	68	16.4	82.0	141272	9	AP001976	Homo sapi	c	141	15.8	79.0	2018	3	AY113567
C	69	16.4	82.0	144383	8	AC092780	Oryza sat	c	142	15.8	79.0	2282	9	BC000148
C	70	16.4	82.0	148501	9	BX284929	Human DNA	c	143	15.8	79.0	2285	8	AK118438
C	71	16.4	82.0	1503884	2	AC005147	Danio rer	c	144	15.8	79.0	2302	9	BC003686
C	72	16.4	82.0	150946	8	AC091246	Oryza sat	c	145	15.8	79.0	2324	9	BC022890
C	73	16.4	82.0	152858	9	AC093428	Oryza sat	c	146	15.8	79.0	2712	7	BRU34036
C	74	16.4	82.0	154937	2	AP002382	Homo sapi	c	147	15.8	79.0	2963	3	AF431855
C	75	16.4	82.0	159198	2	AP004865	Oryza sat	c	148	15.8	79.0	3021	3	AP159136
C	76	16.4	82.0	159736	10	AC122292	Mus muscu	c	149	15.8	79.0	4039	14	HSBE2A
C	77	16.4	82.0	161348	10	AL65532	Mouse DNA	c	150	15.8	79.0	5874	3	AL159137S2
C	78	16.4	82.0	164502	2	AC026960	Homo sapi	c	151	15.8	79.0	10671	1	AB007842
C	79	16.4	82.0	167084	9	AC092999	Homo sapi	c	152	15.8	79.0	11034	14	AF104985
C	80	16.4	82.0	168552	9	AP004891	Oryza sat	c	153	15.8	79.0	15033	2	AC018888
C	81	16.4	82.0	168875	9	AC114794	Homo sapi	c	154	15.8	79.0	18900	9	AY037272
C	82	16.4	82.0	169232	2	AC024299	Homo sapi	c	155	15.8	79.0	20149	8	CNS8CTM
C	83	16.4	82.0	170212	9	AC058822	Homo sapi	c	156	15.8	79.0	24006	2	AC014743
C	84	16.4	82.0	177878	2	BX468995	Danio rer	c	157	15.8	79.0	29545	9	AC112696
C	85	16.4	82.0	178367	2	AC016114	Homo sapi	c	158	15.8	79.0	30583	2	AC017314
C	86	16.4	82.0	181123	2	AC104064	Homo sapi	c	159	15.8	79.0	35560	2	AC127494
C	87	16.4	82.0	182603	9	AF127019	Homo sapi	c	160	15.8	79.0	50374	2	AC015170
C	88	16.4	82.0	185768	10	AC012173	Mus muscu	c	161	15.8	79.0	50607	3	AC00598
C	89	16.4	82.0	187131	2	AP001535	Homo sapi	c	162	15.8	79.0	57287	9	AC00883
C	90	16.4	82.0	189927	10	AC120136	Mus muscu	c	163	15.8	79.0	61173	1	AY37454
C	91	16.4	82.0	189949	2	AC112660	Mus muscu	c	164	15.8	79.0	61532	2	AC143396
C	92	16.4	82.0	192330	2	AC022065	Homo sapi	c	165	15.8	79.0	61532	2	AC143396
C	93	16.4	82.0	194518	9	AC113147	Homo sapi	c	166	15.8	79.0	71396	2	AC113074
C	94	16.4	82.0	194910	9	AC096639	Homo sapi	c	167	15.8	79.0	72987	3	AC00531
C	95	16.4	82.0	195027	2	AC026611	Homo sapi	c	168	15.8	79.0	73148	2	AC048349
C	96	16.4	82.0	204860	9	AC083902	Homo sapi	c	169	15.8	79.0	73170	9	AL44068
C	97	16.4	82.0	205594	9	AP002802	Homo sapi	c	170	15.8	79.0	75499	9	HLJ96521
C	98	16.4	82.0	207303	2	AL645562	Homo sapi	c	171	15.8	79.0	86825	2	AC13082
C	99	16.4	82.0	211844	2	AC048370	Homo sapi	c	172	15.8	79.0	90624	10	AL731671
C	100	16.4	82.0	217393	9	AP001122	Homo sapi	c	173	15.8	79.0	90882	9	AL39282
C	101	16.4	82.0	218657	10	AL731843	Mouse DNA	c	174	15.8	79.0	92059	2	AC128823_3
C	102	16.4	82.0	219496	2	AC118698	Mus muscu	c	175	15.8	79.0	92652	8	AC024261
C	103	16.4	82.0	237845	2	AC112433	Rattus no	c	176	15.8	79.0	93296	9	AL136363
C	104	16.4	82.0	243479	2	BX537152	Danio rer	c	177	15.8	79.0	99791	8	CNS071Q0
C	105	16.4	82.0	244441	2	AC098180	Rattus no	c	178	15.8	79.0	102092	2	AC136053
C	106	16.4	82.0	249412	2	AC095097	Rattus no	c	179	15.8	79.0	108873	14	AF138573
C	107	16.4	82.0	250004	2	AC129469	Rattus no	c	180	15.8	79.0	110000	2	AC098193_4
C	108	16.4	82.0	257078	2	AC118300	Rattus no	c	181	15.8	79.0	110000	2	AC122076_2
C	109	16.4	82.0	257784	2	AC118627	Mus muscu	c	182	15.8	79.0	110000	2	AC29472_1
C	110	16.4	82.0	260480	2	AC141647	Mus muscu	c	183	15.8	79.0	112405	9	AC072023
C	111	16.4	82.0	260657	2	AC094371	Rattus no	c	184	15.8	79.0	112528	2	AC140068
C	112	16.4	82.0	27010	10	AF125314	Mus muscu	c	185	15.8	79.0	119974	9	AC018763
C	113	16.4	82.0	27118	8	AF492377	Aegilops	c	186	15.8	79.0	120279	9	AC009401
C	114	16.4	82.0	273784	2	AC1445245	Human DNA	c	187	15.8	79.0	122815	8	AC135563
C	115	16.4	82.0	281705	8	AP005384	Lotus cor	c	188	15.8	79.0	125933	8	AL732586
C	116	16.4	82.0	297864	8	AF006093	Lotus cor	c	189	15.8	79.0	128758	1	AR279106
C	117	16.4	82.0	300000	2	AC008849	Homo sapi	c	190	15.8	79.0	131133	8	AC146683
C	118	16.4	82.0	313419	9	AC113405	Homo sapi	c	191	15.8	79.0	131441	8	AC146683
C	119	16.4	82.0	314815	2	AC113381	Homo sapi	c	192	15.8	79.0	132221	2	AC120201
C	120	16.4	82.0	315895	2	AC102166	Mus muscu	c	193	15.8	79.0	132819	8	AC024118
C	121	16.4	82.0	316703	9	AC022104	Homo sapi	c	194	15.8	79.0	139788	2	AC024118
C	122	16.4	82.0	317101	2	AC119206	Mus muscu	c	195	15.8	79.0	142347	10	AC125456
C	123	16.4	82.0	317942	2	AC022722	Homo sapi	c	196	15.8	79.0	142712	9	AC121275
C	124	16.4	82.0	318792	9	AC098822	Homo sapi	c	197	15.8	79.0	143451	2	AC022195
C	125	16.4	82.0	325164	2	AC104203	Mus muscu	c	198	15.8	79.0	144357	2	AC146685
C	126	16.4	82.0	328632	2	AC114202	Rattus no	c	199	15.8	79.0	145247	10	AC118173
C	127	16.4	82.0	339192	2	AC139513	Mus muscu	c	200	15.8	79.0	146128	9	AC026358
C	128	16.4	82.0	339893	2	AC107521	Rattus no	c	201	15.8	79.0	147376	10	AL607039
C	129	16.4	82.0	350000	2	Z31891	D. melanogaster	c	202	15.8	79.0	149546	8	AC087256
C	130	16.4	82.0	350124	2	BD229387	Human gen	c	203	15.8	79.0	149819	2	AC121091
C	131	16.4	82.0	350806	2	AR380680	Sequence	c	204	15.8	79.0	149960	5	AC144706
C	132	16.4	82.0	350869	2	AR375131	Sequence	c	205	15.8	79.0	150106	2	AC144913
C	133	16.4	82.0	350936	8	AK060174	Oryza sat	c	207	15.8	79.0	150155	8	AL030928
C	134	16.4	82.0	351676	6	AR376767	Sequence	c	208	15.8	79.0	151547	8	AP03312
C	135	16.4	82.0	351900	11	DM10282T	Human gen	c	209	15.8	79.0	151862	10	AC102383
C	136	16.4	82.0	351900	11	AK069322	Oryza sat	c	210	15.8	79.0	152267	10	AL6522967
C	137	16.4	82.0	351908	8	AK102189	Oryza sat	c	211	15.8	79.0	152313	9	AL591594
C	138	16.4	82.0	351908	8	AK071708	Oryza sat	c	212	15.8	79.0	153203	9	AL359812

c	212	15.8	79.0	153307	10	ALB45441	Mouse DNA	285	15.8	79.0	191814	10	AC130541	Mus muscu
c	213	15.8	79.0	153369	9	AC004803	Homo sapi	286	15.8	79.0	191866	9	AL355980	Human DNA
c	214	15.8	79.0	155713	9	BX00347	Zebrafish	287	15.8	79.0	193391	2	AC06824	Homo sapi
c	215	15.8	79.0	155225	2	AC115007	Mus muscu	288	15.8	79.0	194224	5	AL954868	Zebrafish
c	216	15.8	79.0	155310	2	BX51204	Rattus no	289	15.8	79.0	194510	9	AC092956	Homo sapi
c	217	15.8	79.0	155428	2	AL606832	Mouse DNA	290	15.8	79.0	195269	2	AC134458	Mus muscu
c	218	15.8	79.0	155907	9	AC011890	Homo sapi	291	15.8	79.0	195546	2	AC121701	Rattus no
c	219	15.8	79.0	155235	9	AL3556954	Human DNA	292	15.8	79.0	196350	2	BX248319	Danio rer
c	220	15.8	79.0	155305	9	AL355384	Human DNA	293	15.8	79.0	196817	9	AC019209	Homo sapi
c	221	15.8	79.0	155919	9	AL355194	Human DNA	294	15.8	79.0	196983	2	BX323059	Danio rer
c	222	15.8	79.0	155067	9	AL355368	Human DNA	295	15.8	79.0	199289	10	AL772275	zebrafish
c	223	15.8	79.0	155317	9	AL391873	Human DNA	296	15.8	79.0	199894	10	AC115053	Mus muscu
c	224	15.8	79.0	155182	2	AC110650	Homo sapi	297	15.8	79.0	200425	10	AC114549	Mus muscu
c	225	15.8	79.0	155284	9	AL137000	Human DNA	298	15.8	79.0	200634	2	AC016418	Homo sapi
c	226	15.8	79.0	155589	2	AL590557	Homo sapi	299	15.8	79.0	202029	2	BX855594	Mus muscu
c	227	15.8	79.0	155314	3	AC093039	Homo sapi	300	15.8	79.0	203282	10	AC126674	Danio rer
c	228	15.8	79.0	155475	3	AC012051	Homo sapi	301	15.8	79.0	204249	2	AC117423	Homo sapi
c	229	15.8	79.0	155056	2	AC022412	Homo sapi	302	15.8	79.0	204445	2	AC125268	Rattus no
c	230	15.8	79.0	155328	2	AC022185	Homo sapi	303	15.8	79.0	205643	10	AC101052	Homo sapi
c	231	15.8	79.0	155284	9	AL137000	Human DNA	304	15.8	79.0	205643	10	AC101313	Rattus no
c	232	15.8	79.0	155638	2	AC013514	Homo sapi	305	15.8	79.0	206431	2	AL935191	zebrafish
c	233	15.8	79.0	155964	2	AC128313	Rattus no	306	15.8	79.0	206431	2	BX645907	zebrafish
c	234	15.8	79.0	156185	5	BE649507	Homo sapi	307	15.8	79.0	206431	2	AL935336	Mouse DNA
c	235	15.8	79.0	156052	2	AC022412	Homo sapi	308	15.8	79.0	206431	2	AC118862	Rattus no
c	236	15.8	79.0	155560	7	AL130349	Homo sapi	309	15.8	79.0	206431	2	AY303349	Enterobac
c	237	15.8	79.0	156062	9	AL353768	Human DNA	310	15.8	79.0	208367	2	AC142905	Echeneis
c	238	15.8	79.0	156227	9	AC021868	Homo sapi	311	15.8	79.0	208561	9	AC023200	Homo sapi
c	239	15.8	79.0	156599	10	AL935336	Mouse DNA	312	15.8	79.0	209109	9	AC130388	Rattus no
c	240	15.8	79.0	156909	2	AC118862	Homo sapi	313	15.8	79.0	209643	10	AC080018	Danio rer
c	241	15.8	79.0	156158	2	AC121375	Rattus no	314	15.8	79.0	210074	9	AC121376	Rattus no
c	242	15.8	79.0	157004	2	AC006286	Homo sapi	315	15.8	79.0	210322	10	AC102884	Danio rer
c	243	15.8	79.0	157209	4	AC124905	Homo sapi	316	15.8	79.0	210537	2	AC141868	Rattus no
c	244	15.8	79.0	157454	3	AC007137	Drosophili	317	15.8	79.0	211509	9	CNS0929	Drosophili
c	245	15.8	79.0	157520	2	BA470069	Danio rer	318	15.8	79.0	212475	2	AC093021	Homo sapi
c	246	15.8	79.0	157710	2	AC013388	Homo sapi	319	15.8	79.0	213045	2	AC120846	Danio rer
c	247	15.8	79.0	157868	3	AC010118	Drosophili	320	15.8	79.0	214050	2	AC09590	Homo sapi
c	248	15.8	79.0	157900	2	AC0590454	Homo sapi	321	15.8	79.0	214838	9	AC108131	Mus muscu
c	249	15.8	79.0	157974	9	AC092042	Homo sapi	322	15.8	79.0	215294	2	AC117785	Mus muscu
c	250	15.8	79.0	158123	9	AC050809	Homo sapi	323	15.8	79.0	215615	2	AC098139	Rattus no
c	251	15.8	79.0	158247	3	AC006550	Drosophili	324	15.8	79.0	219266	2	AC130080	Rattus no
c	252	15.8	79.0	158695	9	AC058303	Homo sapi	325	15.8	79.0	220367	2	AC120846	Mus muscu
c	253	15.8	79.0	157535	9	AC142305	Pan trogl	326	15.8	79.0	220357	2	AC111951	Rattus no
c	254	15.8	79.0	157672	5	BX248086	Zebrafish	327	15.8	79.0	224136	2	AC13260	Danio rer
c	255	15.8	79.0	157844	9	AC078842	Homo sapi	328	15.8	79.0	224417	2	AC109523	Rattus no
c	256	15.8	79.0	157956	9	AC105383	Homo sapi	329	15.8	79.0	224539	2	AC081379	Danio rer
c	257	15.8	79.0	157522	2	AC0132922	Mus muscu	330	15.8	79.0	226579	10	AC133525	Mus muscu
c	258	15.8	79.0	157528	2	AC101745	Mus muscu	331	15.8	79.0	227155	10	AL732593	Danio rer
c	259	15.8	79.0	157049	2	AC119418	Mouse DNA	332	15.8	79.0	227155	10	AC123953	Mus muscu
c	260	15.8	79.0	157611	10	AC099578	Mus muscu	333	15.8	79.0	227155	10	AC112396	Danio rer
c	261	15.8	79.0	157356	2	AC103356	Homo sapi	334	15.8	79.0	231140	2	AC116231	Rattus no
c	262	15.8	79.0	157583	3	AC105264	Drosophili	335	15.8	79.0	231165	2	AC120231	Rattus no
c	263	15.8	79.0	157852	2	AC091954	Homo sapi	336	15.8	79.0	232320	10	AC121374	Danio rer
c	264	15.8	79.0	158931	3	AC008019	Homo sapi	337	15.8	79.0	233965	2	AC125739	Rattus no
c	265	15.8	79.0	15799	2	AC120237	Rattus no	338	15.8	79.0	234429	9	AF311103	Danio rer
c	266	15.8	79.0	158242	2	AC027620	Homo sapi	339	15.8	79.0	234967	2	AC10380	Rattus no
c	267	15.8	79.0	158485	2	AC141815	Homo sapi	340	15.8	79.0	235008	2	AC119443	Rattus no
c	268	15.8	79.0	158103	2	AC145923	Pan trogl	341	15.8	79.0	235150	2	AC05650	Rattus no
c	269	15.8	79.0	158193	9	AC0018728	Homo sapi	342	15.8	79.0	236832	2	AC119783	Rattus no
c	270	15.8	79.0	158288	2	AC0186443	Homo sapi	343	15.8	79.0	237805	2	AC121047	Rattus no
c	271	15.8	79.0	158192	9	AC1161731	Human DNA	344	15.8	79.0	237850	2	AC130851	Rattus no
c	272	15.8	79.0	156105	10	AC055777	Mus muscu	345	15.8	79.0	239789	2	AC123342	Rattus no
c	273	15.8	79.0	158564	10	AC119816	Mus muscu	346	15.8	79.0	240747	2	AC108339	Rattus no
c	274	15.8	79.0	158415	2	AC023034	Homo sapi	347	15.8	79.0	241000	2	AC121369	Rattus no
c	275	15.8	79.0	158078	9	AC008045	Homo sapi	348	15.8	79.0	241834	2	AC097978	Rattus no
c	276	15.8	79.0	158734	2	AC0160443	Homo sapi	349	15.8	79.0	241899	2	AC121047	Rattus no
c	277	15.8	79.0	158452	9	AC1357055	Human DNA	350	15.8	79.0	242037	2	AC114200	Rattus no
c	278	15.8	79.0	158650	10	AC136091	Homo sapi	351	15.8	79.0	242348	2	AC111361	Rattus no
c	279	15.8	79.0	158732	9	AC023034	Homo sapi	352	15.8	79.0	242386	2	AC098053	Rattus no
c	280	15.8	79.0	158084	9	AC140950	Pan trogl	353	15.8	79.0	242649	2	AC106488	Rattus no
c	281	15.8	79.0	156692	9	AC021979	Homo sapi	354	15.8	79.0	243563	2	AC098187	Rattus no
c	282	15.8	79.0	159887	2	AC113883	Rattus no	355	15.8	79.0	244259	2	AC123226	Rattus no
c	283	15.8	79.0	151239	2	AC010883	Homo sapi	356	15.8	79.0	244948	2	AC106405	Rattus no
c	284	15.8	79.0	151265	2	AC068996	Homo sapi	357	15.8	79.0	249922	2	AC129001	Rattus no

C	358	15.8	79.0	250087	2	AC066931	AC096931 Rattus no	431	15.4	77.0	144901	2	AC125276	Mus muscu
359	15.8	79.0	250425	2	AC125667	Rattus no	432	15.4	77.0	145336	2	AC105166	Mus muscu	
360	15.8	79.0	251173	2	AC115487	Rattus no	433	15.4	77.0	149886	9	AC069256	Homo sapi	
361	15.8	79.0	251478	2	AC105849	Rattus no	434	15.4	77.0	150076	9	AL122126	Human chr	
C	362	15.8	79.0	252602	2	AC091704	Mus muscu	435	15.4	77.0	153046	9	AL59009	Human DNA
C	363	15.8	79.0	256185	2	AC137749	Rattus no	436	15.4	77.0	154334	3	AC010034	Drosophil
C	364	15.8	79.0	257867	3	AC055557	Drosophil	437	15.4	77.0	157979	9	CNS05D94	AL355922 Human chr
C	365	15.8	79.0	258416	2	AC05944	Rattus no	438	15.4	77.0	158375	2	AC080039	AC080039 Homo sapi
C	366	15.8	79.0	258716	2	AC13281	Rattus no	439	15.4	77.0	161602	9	AC022634	AC022634 Homo sapi
C	367	15.8	79.0	260027	3	AC036559	Drosophil	440	15.4	77.0	168835	10	AC121866	AC121866 Mus muscu
C	368	15.8	79.0	273995	3	AC036669	Drosophil	441	15.4	77.0	164932	10	AC121942	Mus muscu
C	369	15.8	79.0	274047	2	AC124087	Rattus no	442	15.4	77.0	166020	2	AC136149	AC136149 Oryza sat
C	370	15.8	79.0	284127	2	AC18719	Rattus no	443	15.4	77.0	166138	9	AC084756	AC084756 Homo sapi
C	371	15.8	79.0	300134	1	AB017211	Rattus no	444	15.4	77.0	166506	2	AC010012	AC010012 Homo sapi
C	372	15.8	79.0	3033191	2	AE003472	Rattus no	445	15.4	77.0	166766	2	AC119682	AC119682 Rattus no
C	373	15.8	79.0	330919	2	AC05296	Drosophil	446	15.4	77.0	168862	2	AC092527	AC092527 Papiano anu
C	380	15.8	79.0	341560	2	AL596304	Homo sapi	447	15.4	77.0	168880	2	AC114315	Homo sapi
C	381	15.4	77.0	1686	2	AC142249	Sequence	448	15.4	77.0	169157	5	AL627256	Zebrafish
C	382	15.4	77.0	2554	6	BDD22696	BD222696 Encodement	449	15.4	77.0	166138	9	AC025240	AC025240 Homo sapi
C	383	15.4	77.0	2876	6	BC048550	Mus muscu	450	15.4	77.0	170466	3	AC010012	AC010012 Homo sapi
C	378	15.4	77.0	895	8	AF252550	Drosophil	451	15.4	77.0	170332	9	AL161728	AL161728 Human DNA
C	379	15.4	77.0	1420	9	AK06285	Homo sapi	452	15.4	77.0	171343	9	AC099776	AC099776 Homo sapi
C	385	15.4	77.0	1686	2	AKU310841	Rattus no	453	15.4	77.0	172295	10	AL845460	AC1421942 Homo sapi
C	386	15.4	77.0	3021	6	AF265704	Staphyloc	454	15.4	77.0	175008	2	AC010770	AC010770 Homo sapi
C	387	15.4	77.0	3021	6	AX145022	Sequence	455	15.4	77.0	173769	10	AL668919	AL668919 Mouse DNA
C	388	15.4	77.0	3391	1	AF269717	Staphyloc	456	15.4	77.0	173962	2	AC123406	AC123406 Homo sapi
C	389	15.4	77.0	4957	6	AX15035	Sequence	457	15.4	77.0	174002	2	AC011720	AC011720 Homo sapi
C	390	15.4	77.0	57144	2	AC010329	Mus muscu	458	15.4	77.0	174393	2	AC011342	AC111342 Rattus no
C	391	15.4	77.0	5768	8	AF19029	Glycine m	459	15.4	77.0	174949	2	AC113300	AC113300 Mus muscu
C	392	15.4	77.0	63753	2	AC09089	Homo sapi	460	15.4	77.0	176365	2	AC022742	AC022742 Homo sapi
C	393	15.4	77.0	64341	10	AL627323	Mouse DNA	461	15.4	77.0	178786	2	AC123336	AC123336 Rattus no
C	394	15.4	77.0	39578	2	AC101097	Mus muscu	462	15.4	77.0	17946	9	AP02088	AP02088 Homo sapi
C	395	15.4	77.0	49976	2	AC025670	Homo sapi	463	15.4	77.0	179621	2	AC026562	AC026562 Homo sapi
C	396	15.4	77.0	57144	2	AC119567	Homo sapi	464	15.4	77.0	176569	5	BX088540	AL6458540 Zebrafish
C	397	15.4	77.0	63753	2	AF226688	Bombyx mo	470	15.4	77.0	178364	9	AL513306	AL513306 Homo sapi
C	398	15.4	77.0	64341	10	AL627323	Mouse DNA	471	15.4	77.0	178999	9	AL589794	AL589794 Homo DNA
C	399	15.4	77.0	65225	2	AC077109	Homo sapi	472	15.4	77.0	179169	2	AC092759	AC092759 Homo sapi
C	400	15.4	77.0	74282	8	AB025606	Arabidops	473	15.4	77.0	179463	2	AC114308	AC114308 Homo sapi
C	401	15.4	77.0	75075	9	AC004948	Homo sapi	474	15.4	77.0	179724	9	AC022690	AC022690 Homo sapi
C	402	15.4	77.0	79556	9	AC119567	Homo sapi	475	15.4	77.0	183297	2	AC009551	AC009551 Homo sapi
C	403	15.4	77.0	80009	3	AF226688	Bombyx mo	476	15.4	77.0	183547	9	AC024483	AC024483 Homo sapi
C	404	15.4	77.0	80695	5	BX05474	BXK63523 Gallus ga	477	15.4	77.0	183917	9	AC098952	AC098952 Homo sapi
C	405	15.4	77.0	89665	2	AC022403	Homo sapi	478	15.4	77.0	184688	9	AC092944	AC092944 Homo sapi
C	406	15.4	77.0	90015	9	AL513264	Human DNA	479	15.4	77.0	185024	2	AC027649	AL596453 Homo sapi
C	407	15.4	77.0	90599	9	AC130275	Medicago	480	15.4	77.0	185369	10	AL671860	AL671860 Mouse DNA
C	408	15.4	77.0	91073	9	AP001093	Homo sapi	481	15.4	77.0	186233	9	AC092329	AC092329 Homo sapi
C	409	15.4	77.0	103177	9	AP000841	Homo sapi	482	15.4	77.0	186253	9	AC020892	AC020892 Homo sapi
C	410	15.4	77.0	106095	2	AC05474	Stenobrachius	483	15.4	77.0	187679	10	AC128663	AC128663 Homo sapi
C	411	15.4	77.0	107093	2	BX665257	Gallus ga	484	15.4	77.0	189461	2	AC118247	AC118247 Mus muscu
C	412	15.4	77.0	110000	2	AC097394	Continuation (2 of	485	15.4	77.0	190718	8	CNS08C77	AL731744 Oryza sat
C	413	15.4	77.0	110000	2	AC125752	Rattus no	486	15.4	77.0	193931	10	AC16486	AC16486 Mus muscu
C	414	15.4	77.0	113024	2	AL442260	Homo sapi	487	15.4	77.0	197288	2	AC131584	AC131584 Mus muscu
C	415	15.4	77.0	113311	2	AC019822	Drosophil	488	15.4	77.0	197679	10	AC128663	AC128663 Homo sapi
C	416	15.4	77.0	114392	2	AC13580	Rattus no	489	15.4	77.0	200500	9	AC093538	AC093538 Homo sapi
C	417	15.4	77.0	116130	9	AC026423	Homo sapi	490	15.4	77.0	201106	2	AC110375	AC110375 Mus muscu
C	418	15.4	77.0	120088	9	AC004865	Homo sapi	491	15.4	77.0	201664	10	MNMHC2977	AL590389 Mouse DNA
C	419	15.4	77.0	126128	9	CNS07Y0	Alus1662	492	15.4	77.0	201986	10	AC006289	AC006289 Mus muscu
C	420	15.4	77.0	128642	9	AC008838	Homo sapi	493	15.4	77.0	202624	2	AC147073	AC147073 Paratrogli
C	421	15.4	77.0	128920	8	AC10871	Oryza sat	494	15.4	77.0	202681	10	AC116877	AC116877 Mus muscu
C	422	15.4	77.0	129355	9	AC004853	Homo sapi	495	15.4	77.0	203633	9	CNS01RHB	AL161668 Human chr
C	423	15.4	77.0	132348	10	CNS07Y0Z	AC026423	496	15.4	77.0	207901	10	AC1590389	AC1590389 Mouse DNA
C	424	15.4	77.0	134411	9	AL512662	Alu13941	497	15.4	77.0	208734	10	AC03001	AC03001 Mus muscu
C	425	15.4	77.0	135338	8	CNS07Y0P	Oryza sat	498	15.4	77.0	211584	10	AC09910	AC09910 Rattus no
C	426	15.4	77.0	136037	9	AC004104	Homo sapi	499	15.4	77.0	211931	10	AC125259	AC125259 Mus muscu
C	427	15.4	77.0	136777	2	AC146976	Strongyl	500	15.4	77.0	211986	10	AC120837	AC120837 Mus muscu
C	428	15.4	77.0	139266	2	AC146775	Medicago	501	15.4	77.0	213491	2	AC128375	AC128375 Rattus no
C	429	15.4	77.0	141428	9	AL139415	Human DNA	502	15.4	77.0	213634	2	AC122360	AC122360 Mus muscu
C	430	15.4	77.0	143812	2	AC021847	Homo sapi	503	15.4	77.0	214225	2	AC121430	AC121430 Rattus no

c	504	15.4	77.0	216568	2	AL731715	c	577	15.2	76.0	1035	6	AX39895
c	505	15.4	77.0	216557	2	AC119342	c	578	15.2	76.0	1273	10	AB008911
c	506	15.4	77.0	216515	2	BX323558	c	579	15.2	76.0	12212	Sequence	AB008911 Mus muscu
c	507	15.4	77.0	220807	2	AC139643	c	580	15.2	76.0	1287	6	BD16432
c	508	15.4	77.0	221952	2	AC098902	c	581	15.2	76.0	1332	10	U11275
c	509	15.4	77.0	223102	2	AC094457	c	582	15.2	76.0	1335	6	AX67039
c	510	15.4	77.0	224498	2	AC131973	c	583	15.2	76.0	1410	6	AX067037
c	511	15.4	77.0	225082	2	AC102806	c	584	15.2	76.0	1417	6	AX813887
c	512	15.4	77.0	226711	2	AC127440	c	585	15.2	76.0	1419	6	AR388495
c	513	15.4	77.0	227029	2	AC125976	c	586	15.2	76.0	1429	5	CHRPACA
c	514	15.4	77.0	228330	10	AC095281	c	587	15.2	76.0	1453	8	AF068934
c	515	15.4	77.0	229784	10	AC1845171	c	588	15.2	76.0	1526	8	AF035700
c	516	15.4	77.0	231175	2	AC094467	c	589	15.2	76.0	1557	14	AF138298
c	517	15.4	77.0	232225	10	AL662876	c	590	15.2	76.0	1659	6	E03827
c	518	15.4	77.0	234477	2	AC162903	c	591	15.2	76.0	1751	8	AF06247
c	519	15.4	77.0	235528	2	AC096222	c	592	15.2	76.0	1827	8	BT001108
c	520	15.4	77.0	239308	2	AC10741	c	593	15.2	76.0	1852	8	AV133701
c	521	15.4	77.0	239559	2	AC125908	c	594	15.2	76.0	2319	10	MUSNPRPA
c	522	15.4	77.0	239570	2	AC137983	c	595	15.2	76.0	2000	6	AX51047
c	523	15.4	77.0	239726	2	AC097728	c	596	15.2	76.0	2161	1	AF411142
c	524	15.4	77.0	241587	2	AC196197	c	597	15.2	76.0	2180	9	AK126453
c	525	15.4	77.0	242686	2	AC103159	c	598	15.2	76.0	2317	8	AF170172
c	526	15.4	77.0	247978	2	AC094450	c	599	15.2	76.0	2319	10	MUSNPRPA
c	527	15.4	77.0	248352	2	AC095542	c	600	15.2	76.0	2368	6	BD218740
c	528	15.4	77.0	252379	2	AC093477	c	601	15.2	76.0	2385	1	BRLCB0B
c	529	15.4	77.0	254295	2	BX663526	c	602	15.2	76.0	2385	6	E03828
c	530	15.4	77.0	254474	2	AC093478	c	603	15.2	76.0	2386	6	AK122570
c	531	15.4	77.0	256779	2	AC105578	c	604	15.2	76.0	2483	10	S89033
c	532	15.4	77.0	257239	2	AC15215	c	605	15.2	76.0	2660	14	AY103920
c	533	15.4	77.0	257405	2	AC135671	c	606	15.2	76.0	2799	10	RNYPEANT
c	534	15.4	77.0	257609	2	AC137477	c	607	15.2	76.0	2810	9	BC021128
c	535	15.4	77.0	259559	2	AC094598	c	608	15.2	76.0	2872	9	BC035072
c	536	15.4	77.0	259591	2	AC122570	c	609	15.2	76.0	2872	9	BD0712
c	537	15.4	77.0	259651	2	AC096018	c	610	15.2	76.0	2932	10	Cholesterol
c	538	15.4	77.0	261665	2	AC095665	c	611	15.2	76.0	3324	9	AK126453
c	539	15.4	77.0	263127	2	AC112327	c	612	15.2	76.0	3593	8	Hom sapi
c	540	15.4	77.0	263388	2	AC094260	c	613	15.2	76.0	3573	8	CHPSRL2
c	541	15.4	77.0	271135	2	AC103217	c	614	15.2	76.0	3657	6	BC01112
c	542	15.4	77.0	274751	2	AC128993	c	615	15.2	76.0	3663	6	Hom sapi
c	543	15.4	77.0	275392	2	AC095977	c	616	15.2	76.0	3762	6	AK126453
c	544	15.4	77.0	275425	2	AC103101	c	617	15.2	76.0	3768	6	AK126453
c	545	15.4	77.0	280495	2	AC095608	c	618	15.2	76.0	3892	6	AK126453
c	546	15.4	77.0	291709	2	AC094701	c	619	15.2	76.0	3892	6	Hom sapi
c	547	15.4	77.0	293116	2	AC131613	c	620	15.2	76.0	3892	6	AK126453
c	548	15.4	77.0	299859	2	AC128993	c	621	15.2	76.0	3912	1	Mustard
c	549	15.4	77.0	300892	1	AC016747	c	622	15.2	76.0	4114	10	REQ24746
c	550	15.4	77.0	308351	1	AE012555	c	623	15.2	76.0	4270	3	Staphylococcus
c	551	15.4	77.0	310857	2	BY000982	c	624	15.2	76.0	4304	10	AE110478
c	552	15.4	77.0	310972	3	AE003474	c	625	15.2	76.0	4330	9	AE052103
c	553	15.4	77.0	335913	6	AK196295	c	626	15.2	76.0	4391	14	ASU13763
c	554	15.4	77.0	335913	6	AK196296	c	627	15.2	76.0	4484	6	ATR19928
c	555	15.4	76.0	3330	6	AR335019	c	628	15.2	76.0	5321	8	Defecti
c	556	15.2	76.0	177	14	XVSVD15A	c	629	15.2	76.0	5327	7	Staphylococci
c	557	15.2	76.0	259	11	G24310	c	630	15.2	76.0	5455	2	AE00077
c	558	15.2	76.0	441	14	XVSVD15C	c	631	15.2	76.0	5561	9	Sequence
c	559	15.2	76.0	441	14	XVSVD15D	c	632	15.2	76.0	5581	6	Sequence
c	560	15.2	76.0	308	6	XVSVD15E	c	633	15.2	76.0	5881	6	Sequence
c	561	15.2	76.0	330	6	XVSVD15F	c	634	15.2	76.0	5881	6	Sequence
c	562	15.2	76.0	366	14	XVSVD15G	c	635	15.2	76.0	5909	9	Sequence
c	563	15.2	76.0	422	11	G24310	c	636	15.2	76.0	5928	9	Sequence
c	564	15.2	76.0	441	14	XVSVD15H	c	637	15.2	76.0	5937	9	Sequence
c	565	15.2	76.0	443	6	XVSVD15I	c	638	15.2	76.0	5957	9	Sequence
c	566	15.2	76.0	450	8	XVSVD15J	c	639	15.2	76.0	5977	9	Sequence
c	567	15.2	76.0	472	6	XVSVD15K	c	640	15.2	76.0	5997	9	Sequence
c	568	15.2	76.0	499	6	XVSVD15L	c	641	15.2	76.0	6017	9	Sequence
c	569	15.2	76.0	564	6	XVSVD15M	c	642	15.2	76.0	6037	9	Sequence
c	570	15.2	76.0	578	6	XVSVD15N	c	643	15.2	76.0	6057	9	Sequence
c	571	15.2	76.0	581	11	XVSVD15P	c	644	15.2	76.0	6077	9	Sequence
c	572	15.2	76.0	608	11	XVSVD15Q	c	645	15.2	76.0	6097	9	Sequence
c	573	15.2	76.0	632	11	XVSVD15R	c	646	15.2	76.0	6117	9	Sequence
c	574	15.2	76.0	677	14	XVSVD15S	c	647	15.2	76.0	6137	9	Sequence
c	575	15.2	76.0	708	6	XVSVD15T	c	648	15.2	76.0	6157	9	Sequence
c	576	15.2	76.0	859	11	XVSVD15U	c	649	15.2	76.0	6177	9	Sequence
c	577	15.2	76.0	859	11	BV065920	c	650	15.2	76.0	6197	9	Sequence
c	578	15.2	76.0	859	11	BV065920	c	651	15.2	76.0	6217	9	Sequence
c	579	15.2	76.0	859	11	BV065920	c	652	15.2	76.0	6237	9	Sequence
c	580	15.2	76.0	859	11	BV065920	c	653	15.2	76.0	6257	9	Sequence
c	581	15.2	76.0	859	11	BV065920	c	654	15.2	76.0	6277	9	Sequence
c	582	15.2	76.0	859	11	BV065920	c	655	15.2	76.0	6297	9	Sequence
c	583	15.2	76.0	859	11	BV065920	c	656	15.2	76.0	6317	9	Sequence
c	584	15.2	76.0	859	11	BV065920	c	657	15.2	76.0	6337	9	Sequence
c	585	15.2	76.0	859	11	BV065920	c	658	15.2	76.0	6357	9	Sequence
c	586	15.2	76.0	859	11	BV065920	c	659	15.2	76.0	6377	9	Sequence
c	587	15.2	76.0	859	11	BV065920	c	660	15.2	76.0	6397	9	Sequence
c	588	15.2	76.0	859	11	BV065920	c	661	15.2	76.0	6417	9	Sequence
c	589	15.2	76.0	859	11	BV065920	c	662	15.2	76.0	6437	9	Sequence
c	590	15.2	76.0	859	11	BV065920	c	663	15.2	76.0	6457	9	Sequence
c	591	15.2	76.0	859	11	BV065920	c	664	15.2	76.0	6477	9	Sequence
c	592	15.2	76.0	859	11	BV065920	c	665	15.2	76.0	6497	9	Sequence
c	593	15.2	76.0	859	11	BV065920	c	666	15.2	76.0	6517	9	Sequence
c	594	15.2	76.0	859	11	BV065920	c	667	15.2	76.0	6537	9	Sequence
c	595	15.2	76.0	859	11	BV065920	c	668	15.2	76.0	6557	9	Sequence
c	596	15.2	76.0	859	11	BV065920	c	669	15.2	76.0	6577		

C	650	15.2	76.0	11162	14	AF473864	c	723	15.2	76.0	116898	10	AL731687		
C	651	15.2	76.0	11167	1	AE01599	c	724	15.2	76.0	116951	9	AC114788	AC114788	Homo sapi
C	652	15.2	76.0	11168	1	AE02222	c	725	15.2	76.0	117226	8	AP06626	AP06626	Oryza sat
C	653	15.2	76.0	11688	1	AE009887	c	726	15.2	76.0	118235	10	AC03060	AC03060	Mus muscu
C	654	15.2	76.0	12132	1	AE008399	c	727	15.2	76.0	118313	9	AC00391	AC00391	Human DNA
C	655	15.2	76.0	13978	1	AB013613	c	728	15.2	76.0	119666	9	HSDB61B2	AL096710	Human DNA
C	656	15.2	76.0	14179	1	AE007053	c	729	15.2	76.0	121961	2	AC050556	AC090556	Homo sapi
C	657	15.2	76.0	14311	6	AR123015	c	730	15.2	76.0	122151	8	NCB23H20	AL66988	Neurospora
C	658	15.2	76.0	14311	6	AR123016	c	731	15.2	76.0	122356	10	AL845310	AL845310	Mouse DNA
C	659	15.2	76.0	16232	2	AC023615	c	732	15.2	76.0	123039	9	AC03087	AC093087	Oryza sat
C	660	15.2	76.0	19300	14	AT327841	c	733	15.2	76.0	123954	8	AC123518	AC123518	African s
C	661	15.2	76.0	20568	2	AC017847	c	734	15.2	76.0	125008	2	AP003546	AP055346	Oryza sat
C	662	15.2	76.0	23109	1	AE008763	c	735	15.2	76.0	127220	10	BX846469	BP2846469	Mouse DNA
C	663	15.2	76.0	23967	2	AC100971	c	736	15.2	76.0	127374	9	AC114788	AC10579	Homo sapi
C	664	15.2	76.0	30975	3	CBRG33D04	c	737	15.2	76.0	127790	9	AC008885	AC08885	Oryza sat
C	671	15.2	76.0	40520	9	AC011513	c	738	15.2	76.0	128580	2	AP05466	AP05466	African s
C	665	15.2	76.0	34051	9	AC104638	c	739	15.2	76.0	128683	2	AC02732	AC2732	Oryza sat
C	666	15.2	76.0	34713	2	BX339329	c	740	15.2	76.0	128757	9	AL339837	AL339837	Oryza sat
C	673	15.2	76.0	36411	1	U00022	c	741	15.2	76.0	128856	2	AC126779	AC126779	Drosophil
C	668	15.2	76.0	36412	6	AR345364	c	742	15.2	76.0	13098	10	AC146865	AC146865	African s
C	670	15.2	76.0	38322	14	AT327839	c	743	15.2	76.0	131427	9	HS37018	HS37018	Caenorhabditis elegans
C	675	15.2	76.0	45289	3	CBRG33N24	c	744	15.2	76.0	131995	14	OPU5930	OPU5930	Human DNA
C	677	15.2	76.0	45298	3	CBRG33D04	c	745	15.2	76.0	133943	9	AC008496	AC08496	Mus muscu
C	678	15.2	76.0	40866	9	AL590393	c	746	15.2	76.0	137347	9	AL334674	AL334674	Human DNA
C	679	15.2	76.0	43593	9	AC022516	c	747	15.2	76.0	137908	10	AL670724	AL670724	Human DNA
C	680	15.2	76.0	44006	9	AC069162	c	748	15.2	76.0	138078	10	AC114788	AC114788	Oryza sat
C	681	15.2	76.0	53826	2	AC145962	c	749	15.2	76.0	138621	9	AP002028	AP002028	Mus muscu
C	688	15.2	76.0	47338	2	T714	c	750	15.2	76.0	138982	2	AC104550	AC104550	Drosophil
C	689	15.2	76.0	47506	2	AC018082	c	751	15.2	76.0	139493	10	AC066602	AC066602	Staphylococcus aureus
C	690	15.2	76.0	49336	1	AC025950	c	752	15.2	76.0	139636	10	AC129050	AC129050	Homo sapi
C	685	15.2	76.0	50152	2	AC015294	c	753	15.2	76.0	141428	10	AP005558	AP005558	Drosophil
C	686	15.2	76.0	51410	9	AC092604	c	754	15.2	76.0	142193	9	AC121253	AC121253	Caenorhabditis elegans
C	687	15.2	76.0	53604	8	AP003081	c	755	15.2	76.0	142291	2	AC023634	AC023634	Arabidopsis thaliana
C	695	15.2	76.0	60919	3	AC005117	c	756	15.2	76.0	142717	2	AC079578	AC079578	Human DNA
C	696	15.2	76.0	61579	9	AL356258	c	757	15.2	76.0	143384	2	AC129050	AC129050	Rattus norvegicus
C	697	15.2	76.0	62794	8	AP003957	c	758	15.2	76.0	143588	10	BX005168	BX005168	Oryza sat
C	698	15.2	76.0	63501	2	AC134974	c	759	15.2	76.0	143687	9	AC010793	AC010793	Homo sapi
C	693	15.2	76.0	63604	8	AC019704	c	760	15.2	76.0	143883	9	CNS189	CNS189	Mus muscu
C	694	15.2	76.0	66919	3	AC131495	c	761	15.2	76.0	144483	2	AC091701	AC091701	Human DNA
C	695	15.2	76.0	70872	2	AC114997	c	762	15.2	76.0	144503	2	AC100744	AC100744	Drosophil
C	696	15.2	76.0	71044	2	AC024368	c	763	15.2	76.0	144681	2	AC184268	AC184268	Human DNA
C	691	15.2	76.0	74512	2	AC100521	c	764	15.2	76.0	144654	2	AC116784	AC116784	Mus muscu
C	697	15.2	76.0	74575	8	AP004787	c	765	15.2	76.0	146504	10	AC012399	AC012399	Oryza sat
C	699	15.2	76.0	78507	2	AC019745	c	772	15.2	76.0	146554	2	AC055605	AC055605	Human DNA
C	700	15.2	76.0	79857	2	AC131495	c	773	15.2	76.0	146699	9	AC112210	AC112210	Drosophil
C	701	15.2	76.0	82059	9	AC130896	c	774	15.2	76.0	146871	2	AC184268	AC184268	Human DNA
C	702	15.2	76.0	91825	2	AC019854	c	775	15.2	76.0	147451	8	AC16722	AC16722	Mus muscu
C	703	15.2	76.0	92562	10	AT732485	c	776	15.2	76.0	147946	2	AC094342	AC094342	Oryza sat
C	704	15.2	76.0	96079	9	AT71717	c	777	15.2	76.0	148320	10	AL772207	AL772207	Human DNA
C	705	15.2	76.0	96598	6	ADK5500	c	778	15.2	76.0	148320	10	AC05124	AC05124	Zebrafish
C	706	15.2	76.0	97902	9	AL596118	c	779	15.2	76.0	149748	2	AC138287	AC138287	Mus muscu
C	707	15.2	76.0	106123	9	AL158015	c	780	15.2	76.0	149844	2	AC146482	AC146482	Human DNA
C	714	15.2	76.0	109770	2	AC073763	c	781	15.2	76.0	149956	2	AC016722	AC016722	Drosophil
C	708	15.2	76.0	110000	2	AC052480	c	782	15.2	76.0	150295	10	AC112342	AC112342	Human DNA
C	710	15.2	76.0	110000	2	AC096079	c	783	15.2	76.0	150855	2	AC021258	AC021258	Oryza sat
C	711	15.2	76.0	110000	2	AC038640	c	784	15.2	76.0	151073	2	AC13624	AC13624	Mus muscu
C	712	15.2	76.0	110000	2	AC038640	c	785	15.2	76.0	151289	2	AC102184	AC102184	Human DNA
C	713	15.2	76.0	110000	2	AC126130	c	786	15.2	76.0	153520	10	AC125520	AC125520	Mus muscu
C	714	15.2	76.0	110000	2	AT572642	c	787	15.2	76.0	153520	10	AC130505	AC130505	Human DNA
C	709	15.2	76.0	110000	2	LMP7CHR25	c	788	15.2	76.0	155647	10	AC112342	AC112342	Oryza sat
C	716	15.2	76.0	110000	6	AR010754	c	789	15.2	76.0	157185	2	AC064798	AC064798	Human DNA
C	717	15.2	76.0	110102	8	ATP28J12	c	790	15.2	76.0	157394	2	AC04874	AC04874	Oryza sat
C	718	15.2	76.0	111354	8	AP003806	c	791	15.2	76.0	158266	9	AC11478	AC11478	Mus muscu
C	719	15.2	76.0	111568	9	AC083908	c	792	15.2	76.0	158315	9	AL160267	AL160267	Human DNA
C	720	15.2	76.0	112855	2	AP003608	c	793	15.2	76.0	158406	9	AC114297	AC114297	Mus muscu
C	721	15.2	76.0	115289	9	AC011490	c	794	15.2	76.0	159070	2	AC12814	AC12814	Oryza sat
C	722	15.2	76.0	116653	2	AP005574	c	795	15.2	76.0	159104	9	AC108925	AC108925	Homo sapi

796 15.2 76.0 159468 2 AC023314  
 c 797 15.2 76.0 159519 9 AC018511  
 c 798 15.2 76.0 159617 9 AC022018  
 799 15.2 76.0 159832 2 AC104199  
 c 800 15.2 76.0 160039 9 AC104851 Homo sapi

**ALIGNMENTS**

**RESULT 1**

AX282880 AX282880 Sequence 3 from Patent WO0174346. 20 bp DNA linear PAT 02-NOV-2001

DEFINITION Accession AX282880 Version AX282880.1 GI:16609856

KEYWORDS SOURCE ORGANISM synthetic construct

REFERENCE AUTHORS TITLE

JOURNAL FEATURES source

Query Match Best Local Similarity 100.0%; Score 20; DB 6; Length 20; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCATACCTGTTGATG 20 Db 1 GGTCCATACTCATGTGATG 20

**RESULT 2**

HSXPAC5/C HSXPAC5 DEFINITION Human Xeroderma Pigmentosum group A correcting (XPAc) gene, exon 6 and partial cds.

ACCESSION VERSION KEYWORDS SEGMENT SOURCE ORGANISM

U10347.1 GI:501113 5 of 5 Homo sapiens (human)

Homo sapiens Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.

REFERENCE AUTHORS TITLE

JOURNAL FEATURES source

Query Match Best Local Similarity 100.0%; Score 20; DB 6; Length 822; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCATACCTGTTGATG 20 Db 743 GGTCCATACTCATGTGATG 724

**ALIGNMENTS**

**RESULT 3**

AR183106/c AR183106 DEFINITION Sequence 8 from patent US 634056. DNA linear PAT 20-APR-2002

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Unknown. Unknown. Unclassified.

REFERENCE AUTHORS TITLE

JOURNAL FEATURES source

Query Match Best Local Similarity 100.0%; Score 20; DB 6; Length 822; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCATACCTGTTGATG 20 Db 743 GGTCCATACTCATGTGATG 724

**RESULT 4**

AR203243/AR203243 DEFINITION Sequence 8 from patent US 636355. DNA linear PAT 20-JUN-2002

ACCESSION

source /organism="Homo sapiens"

VERSION AR203243.1 JOURNAL repair genes  
 KEYWORDS Patent: WO 0174346-A 13 11-OCT-2001;  
 SOURCE Unknown.  
 ORGANISM HYBRIDON, INC. (US)  
 REFERENCE Unclassified.  
 AUTHORS 1. (bases 1 to 822)  
 TITLE McCutchen-Maloney, S. L.  
 FEATURES Chimeric proteins for detection and quantitation of DNA mutations,  
 source DNA sequence variations, DNA damage and DNA mismatches  
 JOURNAL Patent: US 6365355A 02-APR-2002;  
 FEATURES /organism="unknown"  
 source /mol\_type="unassigned DNA"  
 ORIGIN /mol\_type="unassigned DNA"  
 Query Match 100.0%; Score 20; DB 6; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGTCACATCTGTGATG 20  
 Db 743 GGTCACATCTGTGATG 724

RESULT 5 HUMXPAR/c  
 LOCUS AX277000 DEFINITION Sequence 8 from Patent WO0173079. DNA linear PAT 29-OCT-2001  
 ACCESSION AX277000 VERSION AX277000.1 GI:16548670  
 KEYWORDS Homo sapiens (human)  
 ORGANISM Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE McCutchen-Maloney, S.L.  
 AUTHORS Chimeric proteins for detection and quantitation of dna mutations, dna sequence variations, dna damage and dna mismatches  
 JOURNAL Patent: WO 0173079-A 8 04-OCT-2001; The Regents of The University of California (US)  
 FEATURES Location/Qualifiers 1. .822  
 source /organism="Homo sapiens" /mol\_type="unassigned DNA" /db\_xref="Taxon:9606"

ORIGIN Query Match 100.0%; Score 20; DB 6; Length 822;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGTCATCTGTGATG 20  
 Db 743 GGTCATCTGTGATG 724

RESULT 6 AX282890/c  
 LOCUS AX282890 DEFINITION Sequence 13 from Patent WO0174346. DNA linear PAT 02-NOV-2001  
 ACCESSION AX282890 VERSION AX282890.1 GI:1660886  
 KEYWORDS SOURCE Homo sapiens (human)  
 ORGANISM Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1. .1377  
 AUTHORS Agraval,S. and Kandimalla,E.R.  
 TITLE Sensitization of cells to cytotoxic agents using oligonucleotides directed to nucleotide excision repair or transcription coupled

ORIGIN Query Match 100.0%; Score 20; DB 6; Length 1377;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGTCCATCTGTGATG 20  
 Db 769 GGTCCATCTGTGATG 750

RESULT 7 HUMXPAC  
 LOCUS HUMXPAC DEFINITION Homo sapiens mRNA for XPAC protein, complete cds. ACCESSION D14533  
 VERSION D14533 VERSION D14533.1 GI:286028  
 KEYWORDS SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1. (bases 1 to 1377)  
 AUTHORS Tanaka,K., Miura,N., Satokata,I., Miyamoto,I., Yoshida,M.C., Satoh,Y., Kondo,S., Yasui,A., Okayama,H. and Okada,Y.  
 TITLE Analysis of a human DNA excision repair gene involved in group A xeroderma pigmentosum and containing a zinc-finger domain Nature 348 (6296), 73-76 (1990)  
 JOURNAL MEDLINE  
 PUBLMED 91043046  
 REFERENCE 2  
 AUTHORS Satokata,I., Iwai,K., Matsuda,T., Okada,Y. and Tanaka,K.  
 TITLE Genomic characterization of the human DNA excision repair-controlling gene XPAC  
 JOURNAL MEDLINE  
 PUBLMED 94124028  
 REFERENCE 3  
 AUTHORS (bases 1 to 1377)  
 TITLE Tanaka,K.  
 JOURNAL Direct Submission  
 PUBLMED Submitted (26-FEB-1993) Kiyoshi Tanaka, Osaka University, Inst. for Molecular and Cellular Biology, 1-3 Yamadaoka, Suita, Osaka 565, Japan (Tel:81-6-6877-5238, Fax:81-6-6877-9136)  
 FEATURES Location/Qualifiers 1. .1377  
 source /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="Taxon:9606" /chromosome="9" /clone\_lib="pcD2Basinger" /note "clones pcD2h19 and pcD2h29~human primary fibroblast"  
 gene 1. .1377  
 CDS /gene="XPAC" 27..848  
 /gene="XPAC" /codon\_start=1 /product="XPAC protein" /protein\_id="BA003403\_1" /db\_xref="GI:286029" /translation="MAGADGALPAALEQAPELPASVRSIERRKRALMRQLRLAARPSATATAAGTGGTAAAGTAKPAKPTIDTGGGFTLREEREEBEEQKGVHQPQPMWFDYVICBCKEEMDSYMLDPLPCDNCRDADMKHDKLTKTBAKQEYLUKDCOLEKREPPLKIVKQPHHSQGDMLKLYKLQKIVLWSLEWGSQSRALKEAKEVQENREKMQKKFDKIVKELRRRAVSSWVKRETIYHQHBYGPREENLEDWYRKTCMCGHELTVEK"

ORIGIN

Query Match      100.0%; Score 20; DB 9; Length 1377;  
 Best local similarity 100.0%; Pred. No. 16;  
 Matching 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
GenBank: NM\_001161; mRNA: 34 Row: N Column: 16  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 4507936.  
Location/Qualifiers

Qy	
1	GSTCCATACTCATGTGATG
20	
769	GCTCCATACTCATGTGATG
750	
Db	

```
source
1. .1439
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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		RESULT 8
DEFINITION	Homo sapiens xeroderma pigmentosum, complementation group A, mRNA	BC014965
ACCESSION	(cDNA clone MGC:23059 IMAGE:4878739), complete cds.	BC014965
VERSION	BC014965.1	GI:15929009
KEYWORDS	MGC.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
COMMENT		
FEATURES		
repeat_region	/rpt family="Alu"	
ORIGIN		
REFID		gene
DEFINITION	Xeroderma pigmentosum, complementation group A (XPA)	
ACCESSION	AF503166	
VERSION	AF503166.1	GI:20303097
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 1439)	
AUTHORS	Klauber,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Caminchi,P., Prange,C., Raha,S.S., Loqueta-Lombard,N.A., Peters,G.J., Abramson,R.D., Mulley,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Guaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.R., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krywinski,M.I., Skalska,U., Smilius,D.E., Schnieke,A., Schein,J.E., Jones,J.E., Jones,S.J. and Marra,M.A.	
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
MEDLINE	2238257	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 1439)	
AUTHORS	Strauberg,R.	
TITLE	Direct Submission	
JOURNAL	Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
NIH-MGC Project URL:	<a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	
REMARK	Contact: MGC help desk Email: <a href="mailto:cgbps-@email.nih.gov">cgbps-@email.nih.gov</a>	
COMMENT	Tissue Procurement: Louis Staudt cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada <a href="mailto:info@bcgsc.bc.ca">info@bcgsc.bc.ca</a> Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Heiao, Martin Krywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Seedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Wardy, George Yang, Scott Zuyderduyn, Marco Marra.	
FEATURES		
repeat_region	/rpt family="Alu"	
ORIGIN		
REFID		gene
DEFINITION	Xeroderma pigmentosum, complementation group A (XPA)	
ACCESSION	AF503166	
VERSION	AF503166.1	GI:20303097
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 24994)	
AUTHORS	Rieder,M.J., Braun,A.C., Montoya,M.A., Chung,M.-W., Nguyen,C.P., Nguyen,D.A., Livingston,R.J., Poel,C.L., Robertson,P.D., Schachowitz,W.S., Sherwood,J.K., Wittek,I.A. and Nickerson,D.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-APR-2002) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA	
COMMENT	To cite this work please use: NIEHS-SGP, Environmental Genome Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: <a href="http://egp.gs.washington.edu">http://egp.gs.washington.edu</a> ).	
FEATURES		
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repeat_region 20954. .21262 /note="AluSg repeat: matches 6. .303 of consensus"
repeat_region 21263. .21416 /note="AluSc repeat: matches 132. .285 of consensus"
repeat_region 21417. .21456 /note="20 copies 2 mer ta 92% conserved"
repeat_region 21540. .21839 /note="AluSP repeat: matches 1. .302 of consensus"
repeat_region 22282. .22443 /note="Charlie3 repeat: matches 2531. .2685 of consensus"
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/evidence-not_experimental
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repeat_region 32463. .32508 /note="MER3A repeat: matches 61. .106 of consensus"
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repeat_region 34484. .34613 /note="L2 repeat: matches 2576. .2710 of consensus"
repeat_region 34819. .35010 /note="MER repeat: matches 5. .193 of consensus"
repeat_region 35519. .3507 /note="L2 repeat: matches 2006. .2204 of consensus"
repeat_region 35920. .36229 /note="L2 repeat: matches 2627. .2750 of consensus"
repeat_region 36429. .37325 /note="L1MBB repeat: matches 5258. .6171 of consensus"
repeat_region 37597. .37958 /note="THELIB repeat: matches 1. .364 of consensus"
repeat_region 38790. .38968 /note="AluJo repeat: matches 1. .310 of consensus"
repeat_region 39203. .39497 /note="AluS repeat: matches 1. .175 of consensus"
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repeat_region 41741. .42056 /note="LIME3 repeat: matches 5800. .6155 of consensus"
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repeat_region 42810. .43302 /note="LIME3 repeat: matches 5555. .6074 of consensus"
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repeat_region 4466. .44760 /note="AluSg repeat: matches 2. .306 of consensus"
repeat_region 44908. .45214 /note="AluJo repeat: matches 1. .307 of consensus"
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repeat_region 46001. .46306 /note="AluSg repeat: matches 1. .301 of consensus"
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repeat_region 48578. .48710 /note="FLAM_C repeat: matches 1. .133 of consensus"
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCTCATACATGTGATG 20
Db 5047 GTCCTCATACATGTGATG 5066
repeat_region
COMMENT
REFERENCE
AUTHORS
TITLE
JOURNAL
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarhini; Hominidae; Homo sapiens (human)
Plumb, B.
Plumb, B.
Direct Submission
Submitted (05-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonereques@sanger.ac.uk
On Oct 7, 2000 this sequence version replaced gi:10278028.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba24E19
----- Summary Statistics
Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 18662 bases at least Q40
Consensus quality: 18664 bases at least Q30
Consensus quality: 18664 bases at least Q20
Insert size: 117845; sum-of-contigs
Insert size: 117845; 70.8% error; agarose-fp
Quality coverage: 5.87x in Q20 bases; agarose-fp
coverage: 10.17x in Q20 bases; agarose-fp
----- *
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

```



**FEATURES**

<b>Source</b>	5'-UTR
	CDS
	ORIGIN

Query Match 92.0%; Score 18.4; DB 5; Length 1277;  
 Best Local Similarity 95.0%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0  
 Matches 19; Conservative 0; Mismatches 1;

**QY** 1 GGTCCATACATGTTGATG 20  
**Db** 792 GGTCATACATGTTG 773

**RESULT 1A**  
 AL722555/c

<b>LOCUS</b>	AL722555	DEFINITION	Mouse DNA sequence from clone RP23-124119 on chromosome 4, complete sequence.
<b>ACCESSION</b>	AL722555	<b>VERSION</b>	AL722555.7
<b>KEYWORDS</b>	HTG.	<b>SOURCE</b>	Mus musculus (house mouse)
<b>ORGANISM</b>	Mus musculus		

**REFERENCE** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus .  
**AUTHORS** 1 (bases 1 to 157653)  
**TITLE** Lovell,J.  
**JOURNAL** Direct Submission  
**COMMENT** Submitted (25-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk, humquery@sanger.ac.uk. Clone requests: clonerequest@sanger.ac.uk. On Jul 26, 2002 this sequence version replaced gi:21955637.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: humquery@sanger.ac.uk

-----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the

**FAX:81-6-6879-3119)**

**Suita, Osaka 565, Japan (Tel:81-6-6879-5111 (ex.3211), Locality) Qualifiers**

1. .1277  
 /gene="XPAC"  
 1. .67  
 /gene="XPAC"  
 68. .871  
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 GKDFMDSYLISNHFDIAVCDSCRDABEKKHLJTRTEAKQEVKYLKDQDIDKREPVLFET  
 KKNPNTNTGDMKLUYIKAOVIRKSLEWGSBEALIEEAEKEYRKDNIDMKMKOKKFDFKVEW  
 ELLRTVRSSEWIKKEASGHQHEYGFBEHWEDSYKRCITCCYEMVEM"

3' UTR  
 /gene="XPAC"  
 894. .899  
 /gene="XPAC"  
 1257. .1262  
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 1277  
 /gene="XPAC"

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 10); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Mp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/projects/C_elegans/wormpep) RP23-124I19 is from the RCP1-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowbi,C., Kraft,C.L., Lebow,H., Lefan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshewa,L., Louisseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindarthe,M., Mahmoud,M., Maloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhinney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Primus,E., Pu,L.-L., Plopper,F., Poindexter,A., Popovic,D., Reineke,M., Rieger,M.A., Reigh,R., Ruiz,M., Quirio,J., Rachlin,B., Reeves,K., Regier,M.A., Reigh,R., Morgan,M., Morris,K., Morris,S., Munidas,M., Murphy,M., Nairn,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Ojarnpungsagoon,A., Pal,S., Parks,K., Nakokelneh,O., Okwonuo,G., Olajumppa,G., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sned,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Taylor,C., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Taylor,T., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Williams,G., Wilson,R., Wlezey,R., Wooldren,R., Wei,X., White,F., Wright,D., Wright,R., Wu,J., Yakkub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhao,S., Dunn,D., von Niederhausern,A., Weisz,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G., and Gibbs,R.A.

**TITLE** Direct Submission  
**JOURNAL** Unpublished  
**REFERENCE** 2 (bases 1 to 199263)  
**AUTHORS** Worley,K.C.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (09-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
**COMMENT** 3 (bases 1 to 199263) Rat Genome Sequencing Consortium.  
 Submitted (23-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
 On Sep 19, 2002 this sequence version replaced gi:22953895. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.  
 -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 -----  
 Project Information  
 Center project name: GQB  
 Center clone name: CH230-200512  
 -----  
 Summary Statistics  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 139789 bases at least Q40  
 Consensus quality: 144250 bases at least Q30  
 Consensus quality: 147546 bases at least Q20  
 Estimated insert size: 170133; sum-of-contigs estimation  
 Quality coverage: 3x in Q20 bases; sum-of-contigs estimation  
 -----  
 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a working draft sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.

**FEATURES**  
**source**

**misc\_feature**  
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**ORIGIN**

**misc\_feature**

**RESULT 16**

**AC126180** AC126180

**DEFINITION** 227524 bp DNA linear HTG 13-MAY-2003  
 Rattus norvegicus clone CH230-2008J22, \*\*\* SEQUENCING IN PROGRESS  
 \*\*\*

**ACCESSION** AC126180

**VERSION** AC126180.4

**KEYWORDS** GI:30581548  
 HTGS; HTGS PHASE2; HTGS DRAFT; HTGS\_ENRICHED.

**SOURCE** Rattus norvegicus (Norway rat)

**ORGANISM** Rattus norvegicus

**REFERENCE** Rattus norvegicus (Norway rat)

**AUTHORS** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

**1** (bases 1 to 227524)  
 Muñiz,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anvalaechechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaraanika,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,D., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenes,V., Carter,K., Cavazo,I., Ceasar,H., Centur,A., Chacko,J., Chavez,D., Chen,G., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davis,M.L., Davis,C., Davy-Carroll,L., De Andra,C., Dederich,D., Delgado,O., Denson,S., Demarco,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,D., Durbin,K., Durval,B., Eaves,K., Egan,A., Escottto,M., Eugene,C., Evans,A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,





REFERENCE	2 (bases 1 to 197674)
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE	Direct Submission
JOURNAL	Submitted (19-Nov-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: tsasaki@niasaffrc.go.jp, URL:http://rgp.dnaaffrc.go.jp/ , Tel:81-298-38-7411, Fax:81-298-38-7468)
COMMENT	On Jul 24, 2002 this sequence was replaced by the finished sequence as soon as it is available and the accession number will be preserved.
NOTE:	It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
KEYWORDS	* NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter.
SOURCE	* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
ORGANISM	* by the finished sequence as soon as it is available and the accession number will be preserved.
RESULT 18	1. 197674: contig of 197674 bp in length.
LOCUS	AP00367
DEFINITION	Oriza sativa (japonica cultivar-group) chromosome 1 clone P0696E01, 197674 bp DNA linear HTG 27-NOV-2003
ACCESSION	AP004367
VERSION	AP004367.2
KEYWORDS	*** SEQUENCING IN PROGRESS ***.
SOURCE	HTGS PHASE2.
ORGANISM	Oriza sativa (japonica cultivar-group)
REFERENCE	Oriza sativa (japonica cultivar-group)
AUTHORS	Yamada,C., Harada,C., Hishimoto,M., Honda,M., Ichikawa,Y., Idonuma,A., Iijima,M., Ikeda,M., Ikeno,M., Itoh,S., Itoh,T., Itoh,Y., Itoh,Y., Iwabuchi,A., Kamiya,K., Karasawa,W., Katayose,Y., Kuroda,N., Kuroda,Y., Matsukawa,M., Matsuoka,Y., Miura,T., Nakamura,M., Nakamura,M., Nakashima,M., Nakano,Y., Nakamichi,Y., Nakamura,M., Namiki,N., Negishi,M., Ohta,I., Ono,N., Saji,S., Sakai,K., Shibata,M., Shimokawa,T., Shomura,A., Song,J., Takazaki,Y., Terashawa,K., Tsuchik,K., Waki,K., Yamagata,H., Yamane,H., Yoshikiri,S., Yoshihara,R., Yutaka,K., Zhang,H., Iwama,H., Endo,T., Ito,H., Hahn,J.H., Kim,H.I., Bun,M.Y., Yang,M., Jiang,J. and Gojobori,T.
TITLE	The genome sequence and structure of rice chromosome 1
JOURNAL	Nature 420 (6913), 312-316 (2002)
MEDLINE	2233736
PUBMED	12447438
REFERENCE	1 (bases 1 to 197674)
AUTHORS	Wilson,R.
TITLE	Sequencing of <i>Mus musculus</i>
JOURNAL	Unpublished (2001)
REFERENCE	1 (bases 1 to 198448)
AUTHORS	Abbott,S., Haakenson,W. and Doeber,A.
TITLE	The sequence of <i>Mus musculus</i> BAC clone RP23-84N24
JOURNAL	Unpublished (2001)
REFERENCE	2 (bases 1 to 198448)
AUTHORS	McPherson,J.D. and Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (14-MAR-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE	4 (bases 1 to 198448)
AUTHORS	McPherson,J.D. and Waterston,R.H.
TITLE	Direct Submission
JOURNAL	Submitted (28-MAY-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 198448)  
 AUTHORS McPherson, J.D. and Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 REFERENCE 6 (bases 1 to 198448)  
 AUTHORS Wilson, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 COMMENT On Aug 8, 2002 this sequence version replaced gi:21218509.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu>  
 Contact: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
 ----- Summary Statistics  
 Center project name: M\_BA084N24  
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 NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.  
 This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION: The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.rgsgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:  
 This sequence is the entire insert of the clone. This clone is overlapped by AC122492.

FEATURES Source

- 1. 198448 Location/Qualifiers
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  - /db\_xref="taxon:10090"
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REFERENCE 2 (bases 1 to 190856)  
 AUTHORS DOB Joint Genome Institute.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOB Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 COMMENT On Jun 21, 2000 this sequence version replaced gi:7689973.  
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 mRNA Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: <http://www.jgi.doe.gov>  
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 Qy Db 4 CCATACATGTGATG 20  
 104856 CCATACATGTGATG 104872  
 RESULT 21  
 AC009160/c AC009160 190856 bp DNA linear HTG 21-JUN-2000  
 DEFINITION Homo sapiens chromosome 16 clone RP11-70B3, WORKING DRAFT SEQUENCE,  
 LOCUS 27 unordered pieces.  
 ACCESSION AC009160  
 VERSION AC009160..5  
 KEYWORDS HTG; HTGS PHASB1; HTGS\_DRAFT.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Bacterial; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 190856).  
 AUTHORS DOE Joint Genome Institute.  
 TITLE Sequencing of Human Chromosome 16  
 JOURNAL Unpublished  
 \* 81266: gap of unknown length  
 \* 81365: gap of unknown length  
 \* 81266: contig of 9765 bp in length  
 \* 81267: gap of unknown length  
 \* 81367: contig of 12388 bp in length  
 \* 60754: gap of unknown length  
 \* 60854: gap of unknown length  
 \* 60855: gap of unknown length  
 \* 71401: contig of 10546 bp in length  
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QY	4	CCATACATGATGTGATG 20	
Db	157563	CCATACATGATGTGATG 157547	
KEYWORDS			
SOURCE	Rattus norvegicus	(Norway rat)	
ORGANISM	Rattus norvegicus		
REFERENCE			
AUTHORS	Muzny, D.M., Adams, J., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alshabani, S.L., Amaral, H.C., Are, J.R., Ayotte, M., Banks, T., Barbara, J., Bentzon, J., Bimonte, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burnett, C., Buurrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, T., Christopoulos, C., Cleveland, C.D., Cox, M.D., D'athorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denm, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaij, C., Escott, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gundratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodges, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J.J., Hulyk, S., Hume, J.J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureishi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichatoge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozada, R.J., Luu, A., Lucier, R., Luna, R., Ma, J., Martínez, R., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, R., Massey, E., Mawliney, E., Mcleod, M.P., Meadow, M., Mei, G., Metzker, M., Miner, G., Miner, J., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newsom, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwoenkwo, S., Oghu, M., Okwuonu, G., Oragune, N., Oriodo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L., Quiles, M., Ren, Y.,		
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AUTHORS			
TITLE			
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COMMENT			
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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COMMENT			
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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AUTHORS	Worley, K.C.		
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TITLE	Direct Submission		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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COMMENT			
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
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COMMENT			
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AUTHORS	Worley, K.C.		
TITLE	Direct Submission		
JOURNAL			
COMMENT			
REFERENCE	41 (bases 1 to 253297)		
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VERSION	AC09314.8	On May 9, 2003 this sequence version replaced gi:24942637. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas ( <a href="http://www.hgsc.bcm.edu/projects/rat/">http://www.hgsc.bcm.edu/projects/rat/</a> ). Each contig described in the feature table below represents a scaffold in the Arlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sited gaps filled withNs to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
KEYWORDS	HTGS; HTGS PHASEI; HTGS DRAFT; HTGS_ENRICHED.	Center: Baylor College of Medicine, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
ORGANISM	Rattus norvegicus	3 (bases 1 to 263730)
AUTHORS	Alten, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anvallebechi, V., Aoyagi, A., Ayodele, M., Baden, H., Baldwin, D., Bandaraanake, D., Barker, M., Barnstead, M., Benahmed, F., Bisbal, K., Blair, J., Blakenburgh, K., Blyth, P., Brown, M., Bryant, N., Bulay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Choi, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Crete, A., De Souza, L., Davilla, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Benson, S., Deramo, C., Ding, Y., Dinn, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escott, M., Eugene, S., Evans, C.A., Faills, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, J., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, T., Garza, M., Gebrgeorgegis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guaratina, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.J., Hodgson, A., Hogenes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idalebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapchay, S., Kelly, S., Khan, Z., King, L., Kovar, C., Lai, J., Kowalski, C., Kraft, C.L., Lebow, H., Lievan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewwa, L., Loulseged, H., Loxod, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindarane, M., Mahmoud, M., Mailoy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mahoney, S., McLeod, M., McNeill, T.Z., Meinen, E., Milosavljevic, A., Miner, G., Minji, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, M., Nair, L., Nakervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokelameh, O., Okwoun, G., Olarpunsgoon, A., Pal, S., Parks, K., Patterson, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plipper, F., Poindexter, A., Popovic, D., Prinrus, E., Pu, L.-L., Puozo, M., Quiro, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Rings, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Schwartspeyn, A., Sibson, L., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svarek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Treloar, Z., Usmani, R., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,	
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 260312..262005  
 /note="wgs end\_extension  
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**ORIGIN**  
**Query Match** 85.0%; Score 17; DB 2; Length 263730;  
**Best Local Similarity** 100.0%; **Pred.** No. 8.5e+02;  
**Matches** 17; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;  
**Qy** 1 GGTCCATACTCATGTG 17  
**Db** 167351 GGTCACATCTCATGTG 167335

RESULT 24  
**MMXPAC/C**  
**LOCUS** MMXPAC6 294 bp DNA linear ROD 06-FEB-1997  
**DEFINITION** M.musculus XPAC Xeroderma Pigmentosum group A Correcting gene, exon 6.  
**ACCESSION** X74350  
**VERSION** X74350.1 GI:440563  
**KEYWORDS** Xeroderma Pigmentosum group A Correcting gene (XPAC); Xeroderma  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** Chen,H. and Huang,C.-H.  
**AUTHORS** Chen,H. and Huang,C.-H.  
**JOURNAL** Direct Submission  
**FEATURES** source  
**ORIGIN**  
 Mus musculus (house mouse)  
 A novel spliced form of XPA in the mouse kidney (rhcg)  
 Unpublished  
 2 (bases 1 to 576)  
**REFERENCE** Chen,H. and Huang,C.-H.  
**AUTHORS** Chen,H. and Huang,C.-H.  
**JOURNAL** Submitted (27-FEB-2001) Biochemistry and Molecular Genetics, New York Blood Center, 310 East 67th Street, New York, NY 10021, USA  
**FEATURES** source  
 1. .576  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /tissue\_type="kidney"  
 5' UTR  
 CDS  
 1. .39  
 40. .285  
 /note="XPA; alternatively spliced"  
 /codon\_start=1  
 /product="xeroderma pigmentosum complementation group A"  
 /protein\_id="NP\_031963.1"  
 /db\_xref="GI:19070699"  
 /translation="MDSTIMNHFDLPTCDSCRADDKHLITTEAKQBYLLKDCLDE  
 KREGALREWKPKPRHSQWGDMLKLYLKQVSSKGAGS"  
**REFERENCE** 1 (bases 1 to 294)  
**AUTHORS** van Oosterom,C.T., de Vries,A., Verbeek,S.J., van Kreijl,C.F. and van Steeg,H.  
**TITLE** Cloning and characterization of the mouse XPAC gene  
**JOURNAL** Nucleic Acids Res. 22 (1), 11-14 (1994)  
**MEDLINE** 94173654  
**PUBLISHED** 8127648  
**REFERENCE** 2 (bases 1 to 294)  
**AUTHORS** van Steeg,H.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (27-JUL-1993) H. Van Steeg, National Inst of Public Health and Environmental Protection, P O B 1, 3720 BA Bilthoven, NETHERLANDS  
**FEATURES** source  
 1. .294  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="clal29"  
 /db\_xref="txon:10090"  
 /chromosome="4C2"  
 39..>215  
 /useline=X74345:XPAC\_CDS  
 /label=ex6  
 polyA\_signal  
**RESULT** 26  
**MMXPAC/C**  
**LOCUS** MMXPAC7 919 bp mRNA linear ROD 17-MAY-1994  
**DEFINITION** M.musculus mRNA for XPAC Xeroderma Pigmentosum group A Correcting protein.  
**ACCESSION** X74351  
**VERSION** X74351.1 GI:440564  
**KEYWORDS** Xeroderma Pigmentosum group A Correcting protein (XPAC); Xeroderma  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 938)

**AUTHORS** van Oostrom,C.T., de Vries,A., Verbeek,S.J., van Kreijl,C.F. and van Steeg,H.

**TITLE** Cloning and characterization of the mouse XPAC gene

**JOURNAL** Nucleic Acids Res. 22 (1), 11-14 (1994)

**PUBMED** 8127648

**REFERENCE** 2 (bases 1 to 938)

**AUTHORS** van Steeg,H.

**TITLE** Direct submission

**JOURNAL** Submitted (27-JUL-1993) H. Van Steeg, National Inst of Public Health and, Environmental Protection, P O B 1, 3720 BA Bilthoven, NETHERLANDS

**FEATURES** Location/Qualifiers

**gene**

**CDS**

1. . 938 /organism="Mus musculus", /mol\_type="mRNA" /strain="Ola 129" /db\_xref="taxon:10090" /ce1\_line="embryonic stem cell line E14"

1. . 938 /gene="XPAC Xeroderma pigmentosum group A Correcting gene" 92. . 910 /gene="XPAC Xeroderma pigmentosum group A Correcting gene" /codon\_start=1 /product="XPAC protein" /protein\_id="PRA52393.1", /db\_xref="GO:Q064267", /db\_xref="SWISS-PROT:Q62467"

1. . 938 /db\_xref="PATENT-DBPQVADEPQLPAAVRASVERKRALMIRQARLAAPPYPARATGGSVASVGAQPKNDTKGFLIEBEEBKHEIGNIVHFGPVMEFDYTICBEGKMDSYMLNHFELDPTCISDRADDKHKLTKTEAKQYLLKDCDLEKREPALEFVKKNPRHSQDMKLQKQWVKALEYQSQALEDAKEVRQENREKQKFDDKKUKELRRAIIRRSSVWKRETTTHQHYGPEENLDDMRKTCITCGLHETYK"

**polyA\_signal**

933. . 938 /gene="XPAC xeroderma pigmentosum group A Correcting gene"

**ORIGIN**

Query Match 84.0%; Score 16.8; DB 10; Length 938; Best Local Similarity 90.0%; Pred. No. 7.8e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**Db** 831 GGTCCATATTCTATGTTGGT 812

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**RESULT** 27

**AX566974**

**LOCUS** AX566974 Sequence 173 from Patent WO02077021.

**DEFINITION** DNA linear PAT 29-NOV-2002

**ACCESSION** AX566974

**VERSION** AX566974.1 GI:26001549

**KEYWORDS**

**SOURCE** Streptococcus pneumoniae

**ORGANISM** Streptococcus pneumoniae

**REFERENCE**

1. Authors Malignani,V., Tettelin,H. and Fraser,C.

Title Streptococcus pneumoniae proteins and nucleic acids

Journal Patent: WO 02077021-A 173 03-OCT-2002; THE INSTITUTE FOR GENOMIC RESEARCH (US)

**FEATURES**

**Source**

1. 1029 /organism="Streptococcus pneumoniae" /mol\_type="unassigned DNA" /db\_xref="taxon:1313"

**ORIGIN**

Query Match 84.0%; Score 16.8; DB 6; Length 1029; Best Local Similarity 90.0%; Pred. No. 7.8e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

---

**RESULT** 28

**QY** 1 GGTCCTACTCATGTGTG 20

**Db** 975 GGTCCATGCATGAGTG 994

**REFERENCE**

**AUTHORS** AK115474/C

**LOCUS** Clona intestinalis cDNA, clone:cieg055b24

**DEFINITION** mRNA linear INV 30-NOV-2002

**ACCESSION** AK115474

**VERSION** AK115474.1 GI:3587571

**KEYWORDS** Cliona intestinalis

**SOURCE** Phlebobranchia; Cionidae; Ciona

**ORGANISM** Cliona intestinalis

**REFERENCE**

**AUTHORS** Satou,Y., Yamada,I., Mochizuki,Y., Takatori,N., Kawashima,T., Sasaki,A., Hamaguchi,M., Awazu,S., Yagi,K., Sasakura,Y., Nakayama,A., Ishikawa,H., Inaba,K., and Satoh,N.

**TITLE** A cDNA resource from the basal chordate *Ciona intestinalis* Genesis 33 (4), 153-154 (2002)

**JOURNAL** 22191024

**PUBMED** 12203911

**REFERENCE**

2 (bases 1 to 2138)

**AUTHORS** Satoh,Y. and Satoh,N.

**TITLE** Direct Submission

**JOURNAL** Submitted (04-OCT-2002) Nori Satoh, Kyoto University, Department of Zoology, Sakyō-ku, Kyoto, Kyoto 606-8502, Japan (E-mail: satoh@asidain.kyoto-u.ac.jp, Tel:81-75-753-4095, Fax:81-75-7505-1113)

**COMMENT** Cliona intestinalis cDNA Project (URL: http://ghost.zool.kyoto-u.ac.jp/index1.html).

**FEATURES**

**source**

1. . 2138 /organism="Cliona intestinalis"

/mol\_type="mRNA" /db\_xref="taxon:719" /clone="cieg055b24"

**ORIGIN**

Query Match 84.0%; Score 16.8; DB 3; Length 2138; Best Local Similarity 90.0%; Pred. No. 8.2e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**Db** 1185 GGTCATACTCATGTGTG 20

---

**RESULT** 29

**AE007333/C**

**DEFINITION** Streptococcus pneumoniae TIGR<sub>4</sub> section 16 of 194 of the complete genome.

**ACCESSION** AE007333

**VERSION** AE007333.1 GI:14971638

**KEYWORDS**

**SOURCE** Streptococcus pneumoniae TIGR<sub>4</sub>

**ORGANISM** Streptococcus pneumoniae TIGR<sub>4</sub>

**REFERENCE**

1. (bases 1 to 1134)

**AUTHORS** Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D., Peterson,S., Heidelberg,J., Deboy,R.T., Haft,D.H., Dodson,R.J., Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D., Umayam,L.A., White,O., Salzberg,S.L., Lewis,M.R., Radune,D., Holtzapfel,E., Kouris,H., Wolf,A.M., Utterback,T.R., Hansen,C.L., McDonald,L.A., Feldblyum,T.V., Angiuoli,S., Dickison,T., Hickey,E.K., Holt,I.E., Loftus,B.J., Yang,F., Smith,H.O., Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M.

TITLE	Complete genome sequence of a virulent isolate of <i>Streptococcus pneumoniae</i> 293 (5529), 498-506 (2001)
JOURNAL	Science
MEDLINE	21357209
PUBMED	11463916
REFERENCE	2 (base 1 to 11344)
AUTHORS	Tettelein, H., Nelson, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Peterson, S., Heidelberg, J.F., Deboy, R.T., Raff, D.H., Dodson, R.J., Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.A., White, O., Lewis, M.R., Redine, D., Holtapple, E., Khouri, H., Wolf, M., Utterback, R., Hatten, C.L., McDonald, L.A., Feldblyum, T.V., Angiuoli, S., Gusewan, P., Hickey, E.K., Holt, T.E., Loftus, B.J., Ujwal, M.L., Yang, F., Smith, H.O., Ventur, J.C., Dougherty, B.A., Morrison, D.A., Hollingshead, S.K. and Fraser, C.M.
TITLE	Submitted (29 JUN 2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
JOURNAL	Direct Submission
FEATURES	Location:Qualifiers
source	1. l-1134
gene	/organism="Streptococcus pneumoniae TIGR4" /mol_type="genomic DNA" /strain="TIGR4" /db_xref="taxon:170187" /gene="SP0172" 90. .194 /gene="SP0172" /note="Identified by Glimmer2; putative" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="AAK71353.1" /db_xref="GI:14971639" 255. .224 /translation="MIFIEYTILLPLARDFVVVEGLGSSYVVELFCSF" /transl_table=11 /product="DNA mismatch repair protein HexB" /gene="SP0173" 255. .224 /db_xref="GI:14971540" /codon_start=1 /transl_table=11 /product="DNA mismatch repair protein HexB" /protein_id="AAK74354.1" /db_xref="GI:14971540" /translation="MSHIELPEMANQTAAGEVIERPASIVVVELNIDASSQIT IEERAGLUKVQDINGTAAHDEVELARHATSKIKOADDLIRITNGFRLAPS IASVSLVLTAVDGASHGTIVARGGEHEVIRATPSGTCVKVQDFENTPARKY MKSQAEELHIIIDTVNLRAHIAHPTEPRNSFSISDGEMTRAGTGQLRQAGTGVSA KMKBEIENDSDLFEGTSVFLAEPYVTPQVRISEKEKLMLVSLAANSIKEQILPD MVGRLPLAITHIKDPYLADVNHTQVPIVQKLSLQDGLPGRSGKLU ALENIKSTVNRKEVQETPLKPLNTYKTEKRSRQEDEVQVQVLTDEQQLT LEAKEETLDLTKPAKFEERKPKPANYDQDQHDKLADASIDKAYKLEREASERPELE FFGQMHGTTFAQGRGLMTIQHAQERVKYKTYRSGGNVDSQSQQLJVPYIFFF ADDALRKRRMPLBEVGVFLAEPYVTPQVRISEKEKLMLVSLAANSIKEQILPD EVSTIKYRBLAIMMSKCNKANHRIDDHSSAROLLYLQSQCDNPYCHGRPLVHF TKSMERMRRIQENHTSISRELGY"
gene	/complement(2340. .2432) /gene="SP0174" /complement(2340. .2432) /note="Identified by Glimmer2; putative" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="AAK74355.1" /db_xref="GI:4971641" /transl_table="MVKHNDVDTKTKGKISSKHCPEITKTDVV" /complement(2529. .2996) /gene="SP0175" /complement(2529. .2996) /gene="SP0175" /note="Identified by match to PFAM protein family HMM" /codon_start=1
gene	/product="riboflavin synthase, beta subunit" /protein_id="AAK4356.1" /db_xref="GI:14971642" /transl_table="MNTYVEGNVANNTKIGIYWARNEFITSKLSGALDNLRRENTN EKOEIVAVKPGAREIPLTAKSKAKSKKIDAIICLGATIRGNISHDVCSERSKGIAQ ISLNSELIPMEGVTIDTIEQ1ERAGTAKAGNKGSCKQATEVMNLRTLDA" complement(2997. .4202) /gene="SP0176" /complement(2997. .4202) /note="Identified by match to PFAM protein family HMM" /protein_id="AAK4357.1" /db_xref="GI:14971643" /codon_start=1 /transl_table=11 /product="3,4-dihydroxy-2-butanone 4-phosphate synthase/Cytochrome c oxidase II" /protein_id="AAK4357.1" /db_xref="GI:14971643" /transl_table=11 /product="3,4-dihydroxy-2-butanone 4-phosphate synthase/Cytochrome c oxidase II" /protein_id="AAK4357.1" /db_xref="GI:14971643" /transl_table=11 /product="NFKMVEVSGVLLYLRQSRGKGGLQKLNKUKAYHQDQGMTDLANKLAFGEGDIREVHT GARNMKDQGQSHLTLNNPDRKGIGKQFQLEKYGITISSRISIELEANPYSFYLETKNRM GHILNMEK" complement(4222. .4857) /gene="SP0177" /complement(4222. .4857) /gene="SP0177" /note="Identified by match to TIGR protein family HMM TIGR0018" /codon_start=1 /transl_table=11 /product="riboflavin synthase, alpha subunit" /protein_id="AAK4358.1" /db_xref="GI:14971644" /translation="MFTGILIEEGKVERIQKDSRNCKUSIKASKLTDIHLGDSIAVN GICLUTVTHENHOFTVDUNNETNSRSTAFTLTKGSEVNLERASVNGRUGHVTGHT DGTKTSISKDNNAWVQINTQKELLDILVKGKSYTGDGILTUVKSYKUVPNSVSI PHTEQTIKSKQVGTQVNLENDLIGKVQKLMNDNSPKSEISKELYQNGF" complement(4342. .5942) /gene="SP0178" /complement(4842. .5942) /gene="SP0178" /note="Identified by match to TIGR protein family HMM TIGR0326" /codon_start=1 /transl_table=11 /product="riboflavin biosynthesis protein RibD" /protein_id="AAK74359.1" /db_xref="GI:14971645" /translation="MSDSKMKLAIKLAQKAGGVNPNDMVAVIVKVKDNHIGOGYHE FEGGPHAEINAKNCOKCRESVGATYVLTUPCCCHGKTPRCIDAIIDSGTTRVWVSGD CNPVUSGSKILBENLQVCGILNECLNQKPKVTKVYVPMKVNAMGK LTKNQSKWITEBARKHWHQRHVSAMVGNTVQODPLTCRUEKGKPRIT CDTHTRPSTSKEVTKVANDIKTYTATSEBDKNKKLYKHNGCELSIKKKGGNHDLSS LMOHIGNMQIDSLSLIGSSLMMWSLQQIUDELKIVYIAPKVOFGSKAFPVGGEGISL LMDKIRLKQYAFQSGDNYLIESVYIPCSQE" 6347. .6340 /gene="SP0179" 6347. .6340 /gene="SP0179" /note="Identified by match to PFAM protein family HMM PF003130" /codon_start=1 /transl_table=11 /product="Holliday junction DNA helicase Ruva" /protein_id="AAK74360.1" /db_xref="GI:14971646" /translation="MAYVKGIIITKATVIVLNGCYILHVNAPVYASQGVNQEA QIVVQVREDAHILYFSEDECKLFLSLISGGGPUSALATAADDNAGLYQAE /codon_start=1

RESULT 31  
 BD003720/c  
 LOCUS Polynucleotide of *Streptococcus pneumoniae* and sequence.  
 DEFINITION BD003720  
 VERSION BD003720\_1 GI:1861681  
 KEYWORDS JP 2001501833-A/40.  
 ORGANISM unidentified  
 /unclassified.  
 COMMENT 1 (bases 1 to 14273)  
 AUTHORS Kunsch, C.A., Choi, G.H., Dillon, P.J., Rosen, C.A., Bara, S.C.,  
 Fannion, M. and Dougherty, B.A.  
 TITLE Polynucleotide of *Streptococcus pneumoniae* and sequence  
 JOURNAL Patent: JP 2001501833-A 40 13-FEB-2001;  
 HUMAN GENOME SCIENCES INC  
 OS Unidentified  
 PI JP 2001501833-A/40  
 PD 13-FEB-2001  
 PC 30-OCT-1997 JP 1998520718  
 PR 31-OCT-1996 US 60/02960  
 PT CHARLES A KUNSCH, GIL H CHOI, PATRICK J DILLON, CRAIG A ROSEN, PI  
 MICHAEL FANNON, BRIAN A DOUGHERTY  
 C12N15/09, A01K67/027, C07K14/315, C07K16/12, C12N1/15, C12N1/19,  
 C12N1/21, C12N1/21  
 PC C12N5/10, C12P21/02, C12Q1/68, G06F17/30, C12N15/00, C12N5/00, PC  
 G06F15/40  
 CC Strandedness: Double;  
 CC Topology: Linear;  
 FH Key Location/Qualifiers  
 FT source 1. .14273  
 FT source 1. .14273  
 FEATURES /organism='Unidentified'.  
 SOURCE  
 ORIGIN  
 QUERY 1. .14273  
 /organism="unidentified"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32644"  
 QRY 1 GGTCACATCTAGTGTGATG 20  
 DB 13385 GGTCACATCTAGTGTGATG 13366  
 RESULT 32  
 HS398A12  
 DEFINITION Human DNA sequence from clone RP3-398A12 on chromosome 6p23-25.1,  
 complete sequence.  
 ACCESSION AL021332  
 VERSION AL021332.1 GI:2804159  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Bacteria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 9169)  
 AUTHORS Williams, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk  
 COMMENT Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk

every Match 84.0%; Score 16.8; DB 1; Length 11344;  
 tches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 GGTCACATCTAGTGTGATG 20  
 8381 GGTCACATCTAGTGTGATG 8362

LT 30  
 8808/c  
 NATION Sequence 40 from patent US 6420135. DNA linear PAT 25-SEP-2002  
 ISSION AR218808 AR218808.1 GI:23319742

ACE Unknown.  
 ORGANISM Unclassified.  
 1 (bases 1 to 14273)  
 AUTHORS Kunisch, C.A., Choi, G.H., Dillon, P.S., Rosen, C.A., Barash, S.C.,  
 Fannion, M.R. and Dougherty, B.A.  
 TITLE Streptococcus pneumoniae polynucleotides and sequences  
 JURNAL Patent: US 6420135-A 40 16-JUL-2002;  
 TURES Location/Qualifiers  
 source 1. .14273  
 /organism="unknown"  
 /mol\_type="genomic DNA"  
 IN

every Match 84.0%; Score 16.8; DB 6; Length 14273;  
 tches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 1 GGTCACATCTAGTGTGATG 20  
 13385 GGTCACATCTAGTGTGATG 13366

1st Local Similarity 90.0%; Pred. No. 9.1e+02;  
 1st Local Similarity 90.0%; Pred. No. 9.1e+02;



Db ||||| ||||| ||||| |||||  
49662 GGTCTAATCATGATGATG 49643

Contact: hunquery@sanger.ac.uk

RESULT 35  
AP003965/c

LOCUS AP003965 121852 bp DNA linear PRI 15-MAR-2003  
DEFINITION Homo sapiens genomic DNA, chromosome 11q, clone:CMB9-3109, complete  
sequence.

ACCESSION AP003965  
VERSION AP003965.2 GI:17426130

KEYWORDS HTG;  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Deog,P.,  
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE JOURNAL Published Only in Database (2001)

REFERENCE AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Deog,P.,  
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE JOURNAL Direct Submission  
Submitted (27-JUL-2001) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehito-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:hattori@gsc.riken.go.jp, URL:<http://hgp.gsc.riken.go.jp/>,  
Tel: +81-45-503-9111, Fax: +81-45-503-9170)  
On Dec 7, 2001 this sequence version replaced gi:15027546.

COMMENT FEATURES source  
source 1. 121852  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="11"  
/map="11q"  
/clone="CMB9-3109"

#### ORIGIN

RESULT 36  
HS326L13/c

LOCUS HS326L13 127247 bp DNA linear PRI 07-AUG-2003  
DEFINITION Human DNA sequence from clone RP3-326L13 on chromosome Xq21.1,  
complete sequence.

ACCESSION ZB2170  
VERSION ZB2170.2 GI:33504458

KEYWORDS HTG.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bulkyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE AUTHORS 1 (bases 1 to 127247)  
Graham,D.  
TITLE JOURNAL Direct Submission  
Submitted (07-AUG-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
[hunquery@sanger.ac.uk](mailto:hunquery@sanger.ac.uk) Clone requests: [clonerrequest@sanger.ac.uk](mailto:clonerrequest@sanger.ac.uk)  
COMMENT On Aug 7, 2003 this sequence version replaced gi:1730463.  
--- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
web site: <http://www.sanger.ac.uk>

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL, EMBL\_Sw., SWISSPROT, Tr., TREMBL, Wp., WORMPBP, Information on the WORMBP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep). This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.Sanger.ac.uk/HGP/Chrx>. RPI-326L13 is from the library RPCI-3 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPRC2.  
FEATURES Location/Qualifiers  
source 1. 127247  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="RZPD:RPCI704L13326"  
/chromosome="X"  
/map="q21.1"  
/clone="RP3-326L13"  
/clone\_lib="RPCI-3"

#### ORIGIN

RESULT 37  
AP003886

LOCUS AP003886 129300 bp DNA linear PLN 21-AUG-2003  
DEFINITION Orzya sativa (japonica cultivar-group) genomic DNA, chromosome 8,  
BAC clone:OJ163\_G08, complete sequence.

ACCESSION AP003886  
VERSION AP003886.2 GI:34013497

KEYWORDS HTG.

SOURCE ORZYA SATIVA (japonica cultivar-group)  
Homo sapiens  
Bulkyota; Viridiplanta; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrartoideae; Oryzeae; Oryza.  
REFERENCE AUTHORS 1  
Sasaki,T., Matsumoto,T. and Yamamoto,K.  
Oryza sativa nippobare(GA3) genomic DNA, chromosome 8, BAC  
clone:OJ163\_G08  
Published Only in Database (2001)

REFERENCE AUTHORS 2 (bases 1 to 129300)  
Sasaki,T., Matsumoto,T. and Yamamoto,K.  
TITLE JOURNAL Direct Submission  
Submitted (09-JUN-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai

	AUTHORS	Wilson, R.
	TITLE	Direct Submission
	JOURNAL	Submitted (08-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT	On Jun 4, 2002 this sequence version replaced gi:2085776. The orientation of the sequence is from MIRrev to -1M13 of the BAC clone. The nucleotide sequence of this BAC clone was generated by combining Monarto and RGP-Japan sequencing data.	
FEATURES	Location/Qualifiers	Location/Qualifiers
source	1. 1-129300	/organism="Oryza sativa (japonica cultivar-group)"
		/mol_type="genomic DNA"
		/cultivar="Nipponbare"
		/db_xref="taxon:39947"
		/chromosome="8"
		/clone="O41163_G08"
ORIGIN	Query Match	84.0%; Score 16.8; DB 8; Length 129300;
	Best Local Similarity	90.0%; Pred. No. 1e+03;
	DEFINITION	Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy	Qy	1 GGTCCATACTCATGTTGATG 20
Db	122538	G   T   G   A   C   T   A   G 122557
SOURCE	ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	LOCUS	AC002089 148416 bp DNA linear PRI 08-OCT-2003
AUTHORS	DEFINITION	Homo sapiens BAC clone CTA-308B22 from 7, complete sequence.
TITLE	ACCESSION	AC002089
JOURNAL	VERSION	AC002089.2 GI:21322223
KEYWORDS	HTG.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	PIBMED	9847074
AUTHORS	2 (bases 1 to 148416)	
TITLE	PIBMED	
JOURNAL	AUTHORS	Hawkins, M. and Wollam, A.
REFERENCE	TITLE	The sequence of Homo sapiens BAC clone CTA-308B22
AUTHORS	JOURNAL	Unpublished (2001)
REFERENCE	3 (bases 1 to 148416)	
AUTHORS	WATERSTON, R.	
TITLE	REFERENCE	Waterson, N. Direct Submission
JOURNAL	4 (bases 1 to 148416)	
REFERENCE	AUTHORS	Waterson, N. Direct Submission
JOURNAL	5 (bases 1 to 148416)	
REFERENCE	AUTHORS	Waterson, N. Direct Submission
JOURNAL	6 (bases 1 to 148416)	
REFERENCE	AUTHORS	Waterson, N. Direct Submission
JOURNAL	7 (bases 1 to 148416)	
REFERENCE	AUTHORS	Waterson, N. Direct Submission
JOURNAL	8 (bases 1 to 148416)	
REFERENCE		
	FEATURES	
source	NEIGHBORING SEQUENCE INFORMATION:	Actual start of this clone is at base position 1 of CTA-308B22. Actual end is at base position 148416 of CTA-308B22.
	Location/Qualifiers	Location/Qualifiers
	repeat_region	/clone="CTA-308B22"
	repeat_region	/clone_lib="CITB-HS-A"
	repeat_region	746..970 /rpt_family="MIR"
	repeat_region	1493..2094 /rpt_family="L1"
	repeat_region	/rpt_family="L1"
	repeat_region	2095..3501 /rpt_family="L1"
	repeat_region	3534..3822 /rpt_family="Alu"
	repeat_region	4155..4271 /rpt_family="Alu"
	repeat_region	4284..4335 /rpt_family="Alu"
	repeat_region	/rpt_family="MalR"
	repeat_region	4341..4390 /rpt_family="MalR"
	repeat_region	5095..5484 /rpt_family="L2"
	repeat_region	/rpt_family="L2"
		5575..6074

repeat\_region /rpt\_-family="L1" 6726..6749  
repeat\_region /rpt\_-family="AT\_rich" 6981..7031  
repeat\_region /rpt\_-family="MER103" 7661..7691  
repeat\_region /rpt\_-family="(T)n" 8084..8118  
repeat\_region /rpt\_-family="AT\_rich" 8449..8642  
repeat\_region /rpt\_-family="MTR" 8659..8709  
repeat\_region /rpt\_-family="(CAT)n" 8717..9294  
repeat\_region /rpt\_-family="L1" 9343..9406  
repeat\_region /rpt\_-family="AT\_rich" 9778..10068  
repeat\_region /rpt\_-family="Alu" 10072..10128  
repeat\_region /rpt\_-family="L2" 1010..10217  
repeat\_region /rpt\_-family="AT\_rich" 1030..10560  
repeat\_region /rpt\_-family="L1" 11312..11379  
repeat\_region /rpt\_-family="(TG)n" 11956..12092  
repeat\_region /rpt\_-family="L1" 12534..12548  
repeat\_region /rpt\_-family="AT\_rich" 13448..13780  
repeat\_region /rpt\_-family="L1" 14235..14242  
repeat\_region /rpt\_-family="(A)n" 15057..15212  
repeat\_region /rpt\_-family="MTR" 15451..15741  
repeat\_region /rpt\_-family="Alu" 15850..15884  
repeat\_region /rpt\_-family="AT\_rich" 16142..16424  
repeat\_region /rpt\_-family="L1" 16425..16817  
repeat\_region /rpt\_-family="L1" 16830..17069  
repeat\_region /rpt\_-family="L1" 17070..17369  
repeat\_region /rpt\_-family="Alu" 17370..17610  
repeat\_region /rpt\_-family="L1" 17800..18064  
repeat\_region /rpt\_-family="L1" 18405..18505  
repeat\_region /rpt\_-family="AT\_rich" 19649..19938  
repeat\_region /rpt\_-family="L2" 20337..20661  
repeat\_region /rpt\_-family="MER1\_type" 20779..20822  
repeat\_region /rpt\_-family="MAlR" 20833..21210  
repeat\_region /rpt\_-family="MAlR" 21436..21743  
repeat\_region /rpt\_-family="Alu" 21841..22009  
repeat\_region /rpt\_-family="L1" 22054..22370  
repeat\_region /rpt\_-family="MAlR" 22659..22827  
repeat\_region /rpt\_-family="L1" 24752..24754  
repeat\_region /rpt\_-family="AT\_rich" 26989..26990

---

RESULT 39 AC011144 LOCUS AC011144 DEFINITION Homo sapiens clone RP11-1024, WORKING DRAFT SSEQUENCE, 5 unordered pieces.  
ACCESSION AC011144 VERSION 4 GI:13357401  
KEYWORDS HRC; HRCs PHASE1; HTGS\_DRAFT.  
SOURCE Homo sapiens  
ORGANISM Homo sapiens (human)  
REFERENCE 1 (bases 1 to 152635)  
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukigkitz, B., Brown, A., Castle, M., Colangeli, S., Collymore, M., Cooke, P., Debreuille, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Farreira, P., Fitzgerald, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardiner, S., Grant, G., Haford, A., Horton, J., Howland, J.C., Johnson, R., Jones, C., Kann, J., Karatas, A., Klein, J., Lebockzy, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McSwain, P., McGurk, J., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Strange-Thomann, N., Stojanovic, N., Subramanian, A., Talama, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
COMMENT On March 16, 2001 this sequence version replaced gi:12589337. All repeats were identified using RepeatMasker. Smit, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www-seq.wi.mit.edu>  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center Project name: 12517  
Center clone name: 1\_0\_24  
----- Summary Statistics  
Sequencing vector: M13; M7815; 3% of reads  
Sequencing vector: Plasmid; n/a; 97% of reads  
Chemistry: Dye-terminator  
Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 151169 bases at least Q40  
Consensus quality: 151789 bases at least Q30  
Consensus quality: 152081 bases at least Q20

Insert size: 17000; agarose-fp  
 Insert size: 15225; sum-of-contigs  
 Quality coverage: 6.2 in Q20 bases; agarose-fp  
 Quality coverage: 6.9 in Q20 base.

\* NOTE: This is a "working draft" sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 21727: contig of 21727 bp in length  
 \* 21728 21827: gap of 100 bp  
 \* 21828 69977: contig of 49150 bp in length  
 \* 69978 70077: gap of 100 bp  
 \* 70078 111601: contig of 43524 bp in length  
 \* 111602 111701: gap of 100 bp  
 \* 111702 146223: contig of 34522 bp in length  
 \* 146224 146323: gap of 100 bp  
 \* 146324 152635: contig of 6312 bp in length.

FEATURES  
 SOURCE  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="RPCI-11 Human Male BAC"  
 misc\_feature  
 1. 21727  
 /note="assembly\_fragment:  
 clone\_end=SP6  
 vector\_side:left"  
 21828 . 69977  
 /note="assembly\_fragment"  
 70078 . 111601  
 /note="assembly\_fragment"  
 111602 . 146223  
 /note="assembly\_fragment"  
 146224 . 152635  
 /note="assembly\_fragment  
 clone\_end=17  
 vector\_side:right"

ORIGIN  
 Query Match 84.0%; Score 16.8; DB 2; Length 152635;  
 Best Local Similarity 90.0%; Pred. No. 1e+03; Mismatches 18; Conservative 0; Indels 0; Gaps 0;

Qy 1 GGTCCATCACTATGTTGATG 20  
 Db 7397 GGTCCATGCTCTGTTGATG 7416

RESULT 40  
 AC14044/c  
 LOCUS AC14044 155646 bp DNA linear PRI 18-DEC-2003  
 DEFINITION Pan troglodytes BAC clone RP43-109N23 from 7, complete sequence.  
 ACCESSION AC14044  
 VERSION AC14044.2 GI:38424257  
 KEYWORDS HTG.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1 (bases 1 to 155646)  
 AUTHORS Peacock,C. and Bielecki,I.  
 TITLE Unpublished (2001)  
 JOURNAL 2 (bases 1 to 155646)  
 AUTHORS Wilson,R.  
 TITLE Sequencing of Pan troglodytes  
 JOURNAL Unpublished (2001)  
 REFERENCE 3 (bases 1 to 155646)

AUTHORS Wilson, R. K.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-Aug-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 4 (bases 1 to 155646)  
 REFERENCE  
 AUTHORS Wilson, R. K.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-NOV-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
 5 (bases 1 to 155646)  
 REFERENCE  
 AUTHORS Wilson, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-DEC-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Nov 19, 2003 this sequence version replaced gi:33386996  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu>  
 Contact: [submissions@genome.wustl.edu](mailto:submissions@genome.wustl.edu)  
 ----- Summary Statistics  
 Center project  
 -----  
 1. 152635  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
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 misc\_feature  
 1. 21727  
 /note="assembly\_fragment:  
 clone\_end=SP6  
 vector\_side:left"  
 21828 . 69977  
 /note="assembly\_fragment"  
 70078 . 111601  
 /note="assembly\_fragment"  
 111602 . 146223  
 /note="assembly\_fragment"  
 146224 . 152635  
 /note="assembly\_fragment  
 clone\_end=17  
 vector\_side:right"

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping overlap clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION: Mapping information for this clone was provided by Dr. Web Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:  
 The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes 'Clint', Yerkes #C0471, birthdate: 6-6-80). The clone and detailed information can be obtained from ResGen (<http://www.resgen.com>) or Pieter de Jong and co-workers at <http://www.bacpac.chori.org>.

NEIGHBORING SEQUENCE INFORMATION:  
 This sequence is the entire insert of the clone.  
 Location/Qualifiers  
 SOURCE  
 1. . 155646  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /chromosome="7"  
 /map="7"  
 /clone="RP43-109N23"  
 /clone\_lib="RPCI-43"

ORIGIN  
 Query Match 84.0%; Score 16.8; DB 9; Length 155646;  
 Best Local Similarity 90.0%; Pred. No. 1e+03; Mismatches 18; Conservative 0; Indels 0; Gaps 0;

Qy 1 GGTCCATCACTATGTTGATG 20  
 Db 106829 GGTCCATGCTCTGTTGATG 106810



/db\_xref="GI:8567907"  
 /db\_xref="SPREMBL:Q7XU50"  
 /translation="MLGSGLNLVRAALGFRNTAAFAVFCARFWCARRADASASRP  
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 YKEDDLRKYRICHENHUYCDLWLLQTCPCRISJKELPDKSTVSSAPMSQP  
 PTIPESSVNPTSHFLPVHOBRSHQDGPMPESEVVITIRQ"  
 30110. .30921  
 /gene="OSuNBa0088122.4" Join(3010. .30283,30363. .30683,30769. .30921)  
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 /codon\_start=1  
 /protein\_id="CAD41572.3"  
 /db\_xref="GI:8567908"  
 /db\_xref="SPREMBL:Q7XU19"  
 /translation="MARRVEPDPMWSRSDPCVYLLPPWQORPLYLICGDRQCLMASRN  
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 VTMQRIVLILIAAIFIGGIVNQMRPLIFCGQDQAIAAVETIFASPLVIAQFL  
 HPVRLTYLRTOSINLDTLVCGLATAHLHPLNVWVVLGIGVKAVALASVLANLNL  
 FFLAVYFLKGVKHGRGGFLISAEVPPWVLCVLEWWIEIMILLGCL  
 LINPDTVASMIGLICQTISLIIIFSSLSLSGNSVRSVNSBAGGPEEARATGTVLVL  
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 GSARKDAASINLUSFLYVFLGTPVWMAFWHFLPFRGLNGFLLAQATVNMILVG  
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 /db\_xref="SPREMBL:Q7XU47"  
 /translation="MDEIGPSRSGEAGGDLTSTAREAQORQGAGAVRASQDASPV  
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 SESINQSRGFLPSVTQATATSIWERSRSRSDATTSYVDAKNSDGASTOREVMM  
 LQGRHMWTQMVTRKMGWPWAPLUTSAKINGYTSNFRGKVDTC"  
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 /gene="OSuNBa0088122.7"  
 complement(Join(63664. .64090,65157. .65275,65774. .66067))  
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 /db\_xref="SPREMBL:Q7XU46"  
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 NYRVLALAAADDGSGGCGATCAGSRSCEAMMKETYARCRPTPDDGTEGFWM  
 EKNGCCLCISISSKMAITGDDRYWHSIESTSRFHIVAYLOQIMWLEVAGIDFC  
 FPAGSYSLFLRLQKPKHMGKRYGYESIHGMNJKPTRFOLISDDQCATSYLYLN  
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 /db\_xref="SPREMBL:Q7XU45"  
 /translation="MKEKTLAWNSGILPSARMRDRASRASWVQSLPMTCAVAGTISTLV  
 \* Of the gaps between them are based on estimates that have

MEVHDITGKEKVWCYNAAPYMIENYGCFFEDDVLAQVLOQEIVVOLIQN  
 YCGSSKHNSIPSSYHSGCGERMKYRGEVSYAQLVNDLARELQEMOLASQN  
 IDDENITBHGKTIASSISSSGMAASRSPQQVMEDGDPPDMITYEIQQQGEAIGTE  
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 /protein\_id="CAD41577.3"  
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 /db\_xref="SPREMBL:Q7XU44"  
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 MRRRKRSTASRAPPSPGGRSWTAALSPGAAABERERKRVVKGSSQRIWARGA  
 YDDTNPPKTKQDENTISHVNFEGCSVLRCKAMKTNLANPCASKPYSSEQSPGTPY"  
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 EQTPAGTSDPSVRFNSTGTDGHQVILNRBAGETPKTIPANGTYASINVSPIP  
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 KVATLNFQGAFWLQAVRSQLEQBGTVWSELCKRICKTRPNKDRQOALIROWIKICQTC  
 Qy 1 GGTCCATACTCATGTGATG 20  
 Do 113198 GGTACATACGATGTTAG 113217

RESULT 43  
 SPNEU1908/c  
 LOCUS SPNEU1908  
 DEFINITION Streptococcus pneumoniae clone G54, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 ACCESSION AL49930  
 VERSION 18; Conservative  
 KEYWORDS 0; Mismatches 2; Indels 0; Gaps 0;  
 ORGANISM Streptococcus pneumoniae  
 Bacteria; Firmicutes; Lactobacillales; Streptococaceae;  
 Streptococcus;

REFERENCE  
 AUTHORS Dopazo, J., Mendoza, A., Herrero, J., Caldera, F., Humbert, Y.,  
 Friedl, L., Guerrier, M., Grand-Schenk, E., Gandin, C., de  
 Francesco, M., Polissi, A., Buel, G., Peger, G., Garcia, B., Peitsch, M.  
 and Garcia-Bustos, J.F.

TITLE Annotated draft genomic sequence from a *Streptococcus pneumoniae*  
 type 19F clinical isolate  
 JOURNAL Microb. Drug Resist. 7 (2), 99-125 (2001)  
 MEDLINE 21335329  
 PUBMED 11442348  
 REFERENCE  
 AUTHORS Dopazo, J., Mendoza, A., Herrero, J., Caldera, F., Polissi, A.,  
 Humbert, Y., Friedl, L., Guerrier, M., Grand-Schenk, E., Gandin, C., de  
 Francesco, M., Buel, G., Peger, G., Garcia, B., Peitsch, M. and  
 Garcia-Bustos, J.F.

TITLE Direct Submission  
 JOURNAL Submitted (31-OCT-2000) Research Department, Glaxo Wellcome, S.A.,  
 Severo Ochoa 2, 28760 Tres Cantos, SPAIN  
 COMMENT \* NOTE: This is a "working draft" sequence. It currently  
 \* consists of 1 contig. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have



QY	Db	1 1 GGTCCATACTCATGTTGATG 169662	Query Match 84.0%; Score 16.8; DB 2; Length 186184;
Matches	18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Best Local Similarity 90.0%; Pred. No. 1.1e+03;	
RESULT 45			
AC118611/c			
LOCUS	AC119611	209706 bp	DNA LINEAR HTG 15-NOV-2002
DEFINITION	Rattus norvegicus clone CH230-440C15, WORKING DRAFT		SEQUENCE
ACCESSION	AC119611		
VERSION	AC119611.5		
KEYWORDS	HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
AUTHORS	Muzny, D., Marie, Metzker, M., Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anvallebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrill, K., Calderon, E., Cardenar, V., Carrera, K., Cavazos, I., Cease, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., Di Souza, L., Davis, M.L., Davis, C., Davy-Carroll, L., De Andrade, C., Dederich, P., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escott, M., Eugene, C., Evans, C.A., Fall, T., Fan, G., Fernández-S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frase, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebrgeorgis, E., Geer, K., Gill, R., Grady, M., Guerrini, W., Guaratine, P., Haaland, W., Hamil, C., Hamilton, C., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernández, R., Hines, S., Hlaicin, S.L., Hodgeson, A., Hoque, M., Hollins, B., Howell, S., Huiyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levian, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, Y., Longacre, S., Lopez, J., Lorenshuwa, L., Louisged, H., Izquierdo, R.J., Lu, X., Ma, J., Mankeshwari, M., Manindartne, M., Mahmud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, R., Martinez, E., Mawilney, S., McLeod, M.P., McNeill, T.Z., Meinen, E., Milosavljevic, A., Miner, G., Minia, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundada, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokeluehem, O., Okwuonu, G., Olarinpunbagoo, A., Pal, S., Parks, R., Patterson, S., Paul, H., Perez, A., Perez, L., Pfankoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L., Puzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reutter, M., Richards, S., Riggs, F., Rives, C., Rockey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Saverty, G., Scheier, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sirer, C.D., Smajs, D., Sneed, A., Soergrgen, E., Song, X.-Z., Sorrelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Ustamir, K., Valas, R., Vera, V., Villasana, D., Walord, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., 84999, 85098: gap of unknown length.		



between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded sequenced with an alternate  
chemistry, or covered by high quality data (i.e., phred quality >=  
30); an attempt was made to resolve all sequencing problems, such  
as compressions and repeats; all regions were covered by sequence  
from more than one subclone; and the assembly was confirmed by  
restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,  
Department of Genetics, Washington University, St. Louis MO. For  
additional information about the map position of this sequence, see  
<http://genome.wustl.edu>

#### SOURCE INFORMATION:

The RPCI-23 BAC library has been constructed by Kazutoyo Osegawa  
and Minako Tateno in the laboratory of Pieter de Jong  
(<http://www.chori.org>) from female C57BL/6J mouse kidney and/or  
brain genomic DNA. The clone and detailed information can be  
obtained from Research Genetics, Inc. (<http://www.resgen.com>) or  
Pieter de Jong and coworkers at <http://www.chori.org>

#### NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

#### FEATURES

##### source

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All repeats were identified using RepeatMasker:

Smit, A.P.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence\_submission@genome.wi.mit.edu

Project Information

Center project name: L20349

Center clone name: 331D7

Summary Statistics

Sequencing vector: Plasmid; m/a; 100% of reads

Chemistry: Dye-terminator; Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 223109 bases at least Q40

Consensus quality: 223996 bases at least Q30

Consensus quality: 224258 bases at least Q20

Insert size: 206000; agarose-fp

Quality coverage: 224382; sum-of-contigs

Quality coverage: 8.6 in Q20 bases; agarose-fp

Quality coverage: 7.9 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 9 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submitter.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

\* 1 23106: contig of 2186 bp in length

\* 23187 23286: gap of 100 bp

\* 23287 27308: contig of 4222 bp in length

\* 27309 27408: gap of 100 bp

\* 27409 36046: contig of 8358 bp in length

\* 36047 36146: gap of 100 bp

\* 36147 50755: contig of 14609 bp in length

\* 50756 50855: gap of 100 bp

\* 50856 69982: contig of 19127 bp in length

\* 69983 70032: gap of 100 bp

\* 70083 146450: contig of 73368 bp in length

\* 146451 146550: gap of 100 bp

\* 146551 175621: contig of 20711 bp in length

\* 175622 175722: gap of 100 bp

\* 175722 207711: contig of 33990 bp in length

\* 207712 207811: gap of 100 bp

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RESULT 49

AE016936/c

LOCUS 300340 bp DNA linear BCT 28-MAR-2003

DEFINITION Bacteroides thetaiotaomicron VPI-5482, section 11 of 21 of the

ORGANISM Bacteroides thetaiotaomicron VPI-5482

ACCESSION AE016936 AE015928

REFERENCE AE016936.1 GI:29339725

KEYWORDS

AUTHORS Xu, J., Bjurzell, M.K., Hirmod, J., Deng, S., Carmichael, L.K., Chiang, H.C., Hooper, L.V. and Gordon, J.I.

JOURNAL A Genomic View of the Human-Bacteroides symbiosis

SCIENCE 299 (5615), 2074-2076 (2003)

PUBMED 14663928

REFERENCE 1 (bases 1 to 300340)

AUTHORS Xu, J., Bjurzell, M.K., Hirmod, J., Deng, S., Carmichael, L.K., Chiang, H.C., Hooper, L.V. and Gordon, J.I.

JOURNAL Direct Submission

TITLE Submitted (31-OCT-2002) Department of Molecular Biology and Pharmacology, Washington University in St. Louis, 660 S. Euclid, St. Louis, MO 63110, USA

FEATURES

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 VERSION AX571760.1 GI:26003952  
 KEYWORDS  
 SOURCE Streptococcus pneumoniae  
 ORGANISM Streptococcus pneumoniae  
 Bacteria: Firmicutes; Lactobacillales; Streptococaceae;  
 Streptococcus.  
 REFERENCE 1  
 AUTHORS Massignani,V., Tettelin,H. and Fraser,C.  
 TITLE Streptococcus pneumoniae proteins and nucleic acids  
 JOURNAL Patent: WO 0207021-A 4979 03-OCT-2002;  
 Chiron Sp (IT); THE INSTITUTE FOR GENOMIC RESEARCH (US)  
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Search completed: August 17, 2004, 15:02:53  
 Job time : 1612 secs

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c	163	14.8	74.0	957	6	ABx37681	c	236	14.8	74.0	1836	4	AAk6334
c	164	14.8	74.0	972	6	ABx192762	c	237	14.8	74.0	1836	4	AAk6334
c	165	14.8	74.0	1013	6	ABx192760	c	238	14.8	74.0	1836	4	AAk6334
c	166	14.8	74.0	1051	6	ABx192763	c	239	14.8	74.0	1836	4	AAk6334
c	167	14.8	74.0	1133	7	ABx16086	c	240	14.8	74.0	1836	4	AAk6334
c	168	14.8	74.0	1165	2	AAv08188	c	241	14.8	74.0	1836	4	AAk6334
c	169	14.8	74.0	1165	2	AAv63232	c	242	14.8	74.0	1836	4	AAk6334

c 243	14.8	74.0	126512	6	ABR83429	Abn83429 Human t <sub>ra</sub>	316	14.2	71.0	165	4	AAK20799	Aak20799 Human bra
c 244	14.8	74.0	147724	6	ABR83566	Abn83566 Human cDN	317	14.2	71.0	165	4	ABR846714	Aab846714 Human liv
c 245	14.8	74.0	173810	6	ABR85752	Mouse chr	318	14.2	71.0	165	4	ABR821216	Aab821216 Human gen
c 246	14.8	74.0	178896	6	ABQ88146	Human ost	319	14.2	71.0	170	6	ABX92109	Abx92109 Lung spec
c 247	14.8	74.0	193377	9	ADC35071	Aqc35071 Mouse gen	320	14.2	71.0	209	7	ABX43080	Aab43080 Bovine ES
c 248	14.8	74.0	335199	9	ADC4703	Aqc4703 Human wil	321	14.2	71.0	218	4	AAB34647	Aah34647 Human col
c 249	14.8	74.0	34511	6	ABR55200	Abs55200 Genomic D	322	14.2	71.0	230	2	AAT23211	Aat23211 Human gen
c 250	14.8	74.0	349999	9	ADC87010	Adc87010 Human GPC	323	14.2	71.0	231	3	AAC28393	Aac28393 Human sec
c 251	14.4	72.0	256	4	ABR93045	Abi93045 Rat meas	324	14.2	71.0	234	3	AAB67889	Aaa67889 Pinus rad
c 252	14.4	72.0	392	8	ACM17198	Ach17198 Human adu	325	14.2	71.0	247	4	AAB12630	Aai12630 Probe #12
c 253	14.4	72.0	402	4	ADA89035	Add34944 Human pol	326	14.2	71.0	247	4	AAB67708	Aba67708 Human toe
c 254	14.4	72.0	540	6	ABR68624	Abn68624 Serpco	327	14.2	71.0	247	4	AAB47924	Aai47924 Probe #16
c 261	14.4	72.0	576	4	ASB23940	Aab23940 Human ova	328	14.2	71.0	247	4	ABA49791	Aba49791 Human bre
c 262	14.4	72.0	576	5	ABR82498	Aab82498 Human ova	329	14.2	71.0	247	4	ABA34769	Aba34769 Human #13
c 263	14.4	72.0	1155	6	ABR86166	Novel hum	330	14.2	71.0	247	4	ABA41863	Aaa41863 Human bon
c 264	14.4	72.0	1155	9	ADC15381	Aad15381 Human bre	331	14.2	71.0	247	4	AAB16122	Aak16122 Human bra
c 265	14.4	72.0	1365	6	ADA0035	Ada70035 Rice gene	332	14.2	71.0	247	4	ABA51464	Aab51464 Human liv
c 266	14.4	72.0	1452	3	AAC51127	Aac51127 Arabidps	333	14.2	71.0	247	4	AAB10801	Aab10801 Probe #9
c 267	14.4	72.0	1554	7	ACF72121	Acf72121 Photoclab	334	14.2	71.0	247	6	ABR15800	Abi15800 Human gen
c 268	14.4	72.0	1661	3	ACM3273	Aac3273 Arabidps	335	14.2	71.0	255	5	AABH8259	Aah8259 Rat diffe
c 269	14.4	72.0	1722	7	ADAI1408	Ada11408 Human ova	336	14.2	71.0	283	3	ABA73790	Aab73790 Human pro
c 270	14.4	72.0	1953	4	AKB61012	Aab61012 P. putida	337	14.2	71.0	298	7	ABX42500	Abx42500 Bovine ES
c 271	14.4	72.0	2000	7	ADA73213	Ada73213 Rice gene	338	14.2	71.0	300	2	AABZ14218	Aaz14218 Human gen
c 272	14.4	72.0	2295	3	AAC36218	Aca36218 Prokaryot	339	14.2	71.0	329	2	AABV5297	Aav5297 Staphyloc
c 273	14.4	72.0	2433	2	AAQ89738	Aaq89738 Plasmid	340	14.2	71.0	329	3	ACD71145	Aact71145 Single nu
c 274	14.4	72.0	2437	7	ABT32215	Abt32215 Human neu	341	14.2	71.0	329	3	AAC71148	Aac71148 Single nu
c 275	14.4	72.0	2492	7	ACM32842	Aac32842 Drosophil	342	14.2	71.0	329	3	AAC71265	Aac71265 Single nu
c 276	14.4	72.0	2516	4	ABL25452	Abl25452 Drosophil	343	14.2	71.0	330	4	AAS27147	Aas27147 CDNA enco
c 277	14.4	72.0	2554	3	AAZ29341	Aaz29341 Tomato be	344	14.2	71.0	330	4	AAS30225	Aas30225 DNA encod
c 278	14.4	72.0	2663	2	AAQ89728	Aaq89728 Plasmid	350	14.2	71.0	330	4	AAC5560	Aac5560 Human car
c 279	14.4	72.0	2871	4	ABR20186	Abl20186 Drosophil	352	14.2	71.0	330	5	ACD01880	Acd01880 Human pol
c 280	14.4	72.0	2871	4	ABU22812	Abi22812 Drosophil	353	14.2	71.0	330	9	AABN9325	Abn9325 Enteroococ
c 281	14.4	72.0	2937	7	ABU21888	Abi21888 Drosophil	354	14.2	71.0	330	9	ACB2223	Acb2223 Human ORF
c 282	14.4	72.0	3005	7	AAK9594	Aak9594 MDRT relia	355	14.2	71.0	330	9	ACB19860	Acb19860 Human ner
c 283	14.4	72.0	4062	2	ATA13347	Aat13347 C3G prok	356	14.2	71.0	330	9	ABD1559	Abd1559 Human ner
c 284	14.4	72.0	6094	6	AAQ89496	Aaq89496 Human DNA	358	14.2	71.0	361	5	ABA1559	Aba1559 Human pol
c 285	14.4	72.0	9235	2	AAK13131	Aak13131 Enterococ	359	14.2	71.0	378	2	AABN9285	Abn9285 Staphyloc
c 286	14.4	72.0	9235	6	ABR98926	Ab98926 Enteroococ	360	14.2	71.0	378	6	ABR2923	Abr2923 Human sec
c 287	14.4	72.0	11337	7	ABZ16286	Abz16286 Human mus	361	14.2	71.0	401	4	AAB15814	Aab15814 Probe #57
c 288	14.4	72.0	11337	7	ABZ59274	Abz59274 CDNA exco	362	14.2	71.0	401	4	AAB5827	Aab5827 Human fo
c 289	14.4	72.0	12776	4	ABU11894	Abu11894 Drosophil	363	14.2	71.0	401	4	AAB13628	Aab13628 Probe #63
c 290	14.4	72.0	12878	4	ABU13212	Abu13212 Drosophil	364	14.2	71.0	401	4	AAB13728	Aab13728 Probe #57
c 291	14.4	72.0	16556	2	AAU30787	Aau30787 Alphavirus	370	14.2	71.0	401	4	AAK31752	Aak31752 Human bra
c 292	14.4	72.0	24079	4	AAK71153	Aak71153 Human imm	371	14.2	71.0	401	4	AABK0101	Abk0101 Human bra
c 293	14.4	72.0	24079	7	ABZ67330	Abz67330 Human sec	372	14.2	71.0	401	4	AABK13436	Abk13436 Human liv
c 294	14.4	72.0	24079	7	ABZ73732	Abz73732 Secreted	373	14.2	71.0	401	6	ABD0508	Abd0508 Human gen
c 295	14.4	72.0	24079	7	ADG498437	Adg498437 Human sec	374	14.2	71.0	401	4	AABX39256	Abx39256 Bovine ES
c 296	14.4	72.0	24079	9	ADC20606	Adc20606 Human sec	375	14.2	71.0	401	4	AACB44707	Aacb44707 Human fo
c 297	14.4	72.0	50000	9	ADG60733	Adg60733 Human sli	376	14.2	71.0	405	3	AAC37114	Aac37114 Arabidops
c 298	14.4	72.0	50341	2	ADY22674	Ady22674 DNA seqe	377	14.2	71.0	406	3	AAB10463	Aab10463 Probe #39
c 299	14.4	72.0	50341	3	ADZ239519	Adz239519 L5 shutt	378	14.2	71.0	406	4	ABD05109	Abd05109 Human fo
c 300	14.4	72.0	52297	2	ADT51411	Adt51411 Mycobacte	379	14.2	71.0	406	4	AAB13176	Aab13176 Probe #40
c 301	14.4	72.0	52398	5	AAQ05723	Aaq05723 Human rib	380	14.2	71.0	406	4	AAB21919	Aba21919 Probe #38
c 302	14.4	72.0	67571	7	ADP53224	Adp53224 Continuation (6 of	381	14.2	71.0	406	4	AAB5834	Aab5834 Human bon
c 303	14.4	72.0	75798	7	ABX77212	Abx77212 Mouse uri	382	14.2	71.0	406	4	AABK00391	Aak00391 Human bra
c 304	14.4	72.0	110000	7	ACFR7367	Acf7367_5 Continuation (54 o	383	14.2	71.0	406	4	ABZ85387	Abz85387 Human sec
c 305	14.4	72.0	110000	7	ADB88615	Adb88615 Frizzled	384	14.2	71.0	406	4	AAB13401	Aai13401 Probe #39
c 306	14.2	71.0	23	9	ADT5111	Adt5111 Mycobacte	385	14.2	71.0	406	4	ABD55099	Abd55099 Human fo
c 307	14.2	71.0	33	6	ADL47523	Adl47523 Human rib	386	14.2	71.0	406	4	AAB134756	Aai134756 Probe #34
c 308	14.2	71.0	36	3	ADP20660	Adp20660 Continuation (6 of	387	14.2	71.0	406	4	ABD44645	Aba44645 Human bra
c 309	14.2	71.0	65	6	ABR51703	Abn51703 Mouse spl	388	14.2	71.0	406	4	Aba24848	Aba24848 Probe #33
c 310	14.2	71.0	160	4	ABR9525	Aba9525 Human fo	389	14.2	71.0	406	4	AAB17760	Abs17760 Human gen
c 311	14.2	71.0	160	6	ABR9525	Aba9525 Human gen	390	14.2	71.0	406	4	Aba72733	Aba72733 Human fo
c 312	14.2	71.0	165	4	ABR72737	Aba72737 Probe #21	391	14.2	71.0	406	4	AAB15285	Aab15285 Probe #21
c 313	14.2	71.0	165	4	ABR52785	Aba52785 Probe #21	392	14.2	71.0	406	4	AAB38182	Aba38182 Probe #16
c 314	14.2	71.0	165	4	ABR44645	Aba44645 Human bra	393	14.2	71.0	406	4	AAB46949	Aba46949 Human bon

389	14.2	71.0	484	4	AAX28813	Aak28813 Human bon Aak0362 Human bra	C 462	14.2	71.0	1452	6	ABZ14597	Arabidops Abz13991 Arabidops
390	14.2	71.0	484	4	AAX03362	Aab28422 Human liv Aai0289 Probe #332	C 463	14.2	71.0	1470	6	ABZ13990	Arabidops Abz09909 Human rec
391	14.2	71.0	484	4	AAB28422	Aab28422 Human liv Aai0289 Probe #332	C 464	14.2	71.0	1477	5	AAS80066	DNA encod
392	14.2	71.0	484	5	AAX103289	Aab03343 Human gen Aba57502 Human foie	C 465	14.2	71.0	1481	5	AAS80066	DNA encod
393	14.2	71.0	484	6	AAB503343	Aab03343 Human gen Aai17055 Prob #57	C 466	14.2	71.0	1536	6	ABN70708	Streptococ
394	14.2	71.0	486	4	AAX137055	Aab26990 Probe #54	C 467	14.2	71.0	1574	8	ACD7895	CDNA enco
395	14.2	71.0	486	4	AAB26990	Aba26990 Probe #54	C 469	14.2	71.0	1591	9	ADB69393	C. neofor
396	14.2	71.0	486	4	AAX31148	Aak31148 Human bon	C 470	14.2	71.0	1592	3	AAC77881	Aac73871 Human imm
398	14.2	71.0	486	4	AAX05545	Aak05545 Human bra	C 471	14.2	71.0	1604	4	AAK81317	Aak81317 Human imm
399	14.2	71.0	486	4	AAB28303	Aab28303 Probe #67	C 472	14.2	71.0	1626	6	ABN70294	Streptococ
400	14.2	71.0	486	4	AAB50900	Abs05000 Human gen	C 473	14.2	71.0	1626	6	ABE66277	Streptococ
401	14.2	71.0	493	4	AAH11545	Aah11545 Human CDN	C 474	14.2	71.0	1630	3	AAC5015	Arabidops
402	14.2	71.0	525	4	AAB53240	Aah53240 S. epider	C 475	14.2	71.0	1635	3	AAC5245	Arabidops
403	14.2	71.0	548	4	AAB59332	Aba59332 Human foie	C 476	14.2	71.0	1641	4	AAC59785	Human sec
404	14.2	71.0	548	4	AAT139704	Aai139704 Prob #83	C 477	14.2	71.0	1642	4	ABL10295	Drosophil
410	14.2	71.0	555	9	AOC91108	Aad91108 E. faeciu	C 483	14.2	71.0	1651	6	ACD98388	A. thalha
411	14.2	71.0	562	9	ADG33014	Adg33014 Human mit	C 484	14.2	71.0	1651	9	ADD0367	Add30267 Plant yie
412	14.2	71.0	571	4	AAB35222	Aak33522 Human pro	C 485	14.2	71.0	1651	9	ABX63505	Abx63505 Human CDN
413	14.2	71.0	586	6	ABH66037	Abn66037 Human can	C 486	14.2	71.0	1653	7	ACA439754	Aca39754 Prokaryot
414	14.2	71.0	592	4	AAY79691	Aak79691 Human imm	C 487	14.2	71.0	1661	6	ABN68661	Abn68661 Streptoc
408	14.2	71.0	548	4	AAB8782	Abs08782 Human pro	C 488	14.2	71.0	1661	6	ABN68661	Abn68661 Streptoc
410	14.2	71.0	555	9	AAP09327	Aad91108 E. faeciu	C 489	14.2	71.0	1675	7	ACA43064	Prokaryot
411	14.2	71.0	562	9	ADG33014	Adg33014 Human mit	C 490	14.2	71.0	1679	7	ABX63505	Abx63505 Human CDN
412	14.2	71.0	571	4	AAB35222	Aak33522 Human pro	C 491	14.2	71.0	1679	10	ADE67985	Ad676985 Human CDN
413	14.2	71.0	586	6	ABH66037	Abn66037 Human can	C 492	14.2	71.0	1686	4	AFD24899	Aaf25489 Prokaryot
414	14.2	71.0	592	4	AAY79691	Aak79691 Human imm	C 493	14.2	71.0	1686	5	ADA70920	Ada70920
415	14.2	71.0	600	5	AAY14127	Aby14127 Human pro	C 494	14.2	71.0	1687	7	ABZ26174	Abz26174 Human sec
416	14.2	71.0	629	3	AAP09327	Aaf9327 Fusarium	C 495	14.2	71.0	1689	3	AAC77881	Aac77881 Escherich
417	14.2	71.0	648	4	ABL15187	Abl15187 Drosophil	C 496	14.2	71.0	1695	3	ABQ1798	Abq1798 Ro/SSA au
418	14.2	71.0	657	4	AAB22877	Abl22877 Drosophil	C 497	14.2	71.0	1697	6	ABQ70018	Abq70018 Listeria
419	14.2	71.0	693	7	AAB272013	Abz272013 Human NAD	C 498	14.2	71.0	1708	9	ACD18526	Acd18526 Human pro
420	14.2	71.0	700	4	ABL03751	Abn66037 Human can	C 499	14.2	71.0	1709	6	ABD69393	Abd69393 Streptoc
421	14.2	71.0	721	2	AAT35105	Aat35105 Down-regu	C 500	14.2	71.0	1709	7	ACB21814	Acb21814 Prokaryot
422	14.2	71.0	729	3	AAC53161	Aac53161 Arabidops	C 501	14.2	71.0	1709	7	ABQ51804	Acq51804 DNA encod
423	14.2	71.0	743	6	AACD7903	Acd07003 DNA encod	C 502	14.2	71.0	1709	7	ABD16786	Abd16786 Bacillus
424	14.2	71.0	743	6	AAB137525	Abl137525 Human CDN	C 503	14.2	71.0	1709	3	ABX63505	Abx63505 Human CDN
425	14.2	71.0	771	3	AAC53200	Aac53200 Arabidops	C 504	14.2	71.0	1709	9	ACB21814	Acb21814 Prokaryot
426	14.2	71.0	776	4	AAB15574	Aba15574 Streptoc	C 505	14.2	71.0	1709	9	ACB21814	Acb21814 Prokaryot
427	14.2	71.0	776	4	AAB15574	Aba15574 Human neu	C 506	14.2	71.0	1709	9	ACB21814	Acb21814 Prokaryot
428	14.2	71.0	789	3	AAC53161	Aac53161 Arabidops	C 507	14.2	71.0	1709	7	ABD16786	Abd16786 Bacillus
429	14.2	71.0	801	4	AACD63165	Acd63165 Arabidops	C 508	14.2	71.0	1709	7	ABD16786	Abd16786 Bacillus
430	14.2	71.0	807	2	AAB139942	Aab139942 Fungal me	C 509	14.2	71.0	1709	3	ABX63505	Abx63505 Human CDN
431	14.2	71.0	830	2	AAC216633	Aca216633 Human gen	C 510	14.2	71.0	1709	9	ACD18526	Acd18526 Human pro
432	14.2	71.0	870	7	AAC19785	Aca19785 Prokaryot	C 511	14.2	71.0	1709	9	ACB21814	Acb21814 Prokaryot
433	14.2	71.0	896	5	AAB15574	Aba15574 Human big	C 512	14.2	71.0	1709	9	ACB21814	Acb21814 Prokaryot
434	14.2	71.0	915	7	AAC53161	Aac53161 Prokaryot	C 513	14.2	71.0	1709	7	ABD16786	Abd16786 Bacillus
435	14.2	71.0	917	3	AAC36196	Aca36196 Human	C 514	14.2	71.0	1709	7	ABD16786	Abd16786 Bacillus
436	14.2	71.0	919	6	AAB15803	Abl15803 Plant	C 515	14.2	71.0	1709	3	ACB21814	Acb21814 Prokaryot
437	14.2	71.0	930	7	AAC339461	Aca339461 Prokaryot	C 516	14.2	71.0	1709	7	ACB21814	Acb21814 Prokaryot
438	14.2	71.0	1025	6	AAB137529	Aab137529 Lactobaci	C 517	14.2	71.0	1709	7	ACB21814	Acb21814 Prokaryot
439	14.2	71.0	1059	6	AAB140697	Abl140697 Human big	C 518	14.2	71.0	1709	7	ACB21814	Acb21814 Prokaryot
440	14.2	71.0	1095	4	ABL22477	Abl122477 Drosophil	C 519	14.2	71.0	1709	7	ACB21814	Acb21814 Prokaryot
441	14.2	71.0	1146	7	AAC32818	Aca32818 Prokaryot	C 520	14.2	71.0	1709	7	ACB21814	Acb21814 Prokaryot
442	14.2	71.0	1148	9	AAB130958	Aab130958 Plant	C 521	14.2	71.0	1709	3	ACB21814	Acb21814 Prokaryot
443	14.2	71.0	1176	6	ABD151020	Abd151020 Human RNA	C 522	14.2	71.0	1710	9	ACB21814	Acb21814 Prokaryot
444	14.2	71.0	1176	7	ABD151020	Abd151020 DNA encod	C 523	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
445	14.2	71.0	1192	3	AAC36066	Aca36066 Arabidops	C 524	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
446	14.2	71.0	1213	4	AAB158032	Aab158032 Human sec	C 525	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
447	14.2	71.0	1281	5	AAC290791	Aca290791 CDNA enco	C 526	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
448	14.2	71.0	1287	7	AAC31014	Aca31014 Prokaryot	C 527	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
449	14.2	71.0	1290	9	AAC25205	Aca25205 Human CDN	C 528	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
450	14.2	71.0	1291	5	AAC25205	Aca25205 American	C 529	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
451	14.2	71.0	1291	7	AAC25205	Aca25205 Prokaryot	C 530	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
452	14.2	71.0	1296	7	AAC25205	Aca25205 S. pneumo	C 531	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
453	14.2	71.0	1305	3	AAC54212	Aca54212 Arabidops	C 532	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
454	14.2	71.0	1312	4	AAC108777	Aca108777 Drosophil	C 533	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
455	14.2	71.0	1316	5	AAC25205	Aca25205 Human	C 534	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
456	14.2	71.0	1325	2	AAC25205	Aca25205 DNA encod	C 535	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
457	14.2	71.0	1325	2	AAC25205	Aca25205 RNA encod	C 536	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
458	14.2	71.0	1326	7	AAC25205	Aca25205 Human	C 537	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
459	14.2	71.0	1326	7	AAC25205	Aca25205 Human	C 538	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
460	14.2	71.0	1327	4	AAC25205	Aca25205 Human	C 539	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
461	14.2	71.0	1327	4	AAC25205	Aca25205 Human	C 540	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
462	14.2	71.0	1327	4	AAC25205	Aca25205 Human	C 541	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
463	14.2	71.0	1327	4	AAC25205	Aca25205 Human	C 542	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
464	14.2	71.0	1327	4	AAC25205	Aca25205 Human	C 543	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
465	14.2	71.0	1327	4	AAC25205	Aca25205 Human	C 544	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
466	14.2	71.0	1327	4	AAC25205	Aca25205 Human	C 545	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot
467	14.2	71.0	1327	4	AAC25205	Aca25205 Human	C 546	14.2	71.0	1710	2	ACB21814	Acb21814 Prokaryot

C 535	14.2	71.0	2347	2	AQ03395	14.2	71.0	3222	4	ABL05253
S 536	14.2	71.0	2347	2	AQ03393	R496L	ASM	608	14.2	Abl05253 Drosophil
C 537	14.2	71.0	2347	2	AAT95067	c	609	14.2	Aad41265 Human ade	
S 538	14.2	71.0	2347	2	AAT95063	c	610	14.2	Aad41265 Human ade	
C 539	14.2	71.0	2347	2	AAT95065	c	611	14.2	Aad41265 Human ade	
C 540	14.2	71.0	2347	2	AAT95065	c	612	14.2	Aad41265 Human ade	
C 541	14.2	71.0	2347	8	ACD28697	c	613	14.2	Aad41265 Human ade	
C 542	14.2	71.0	2347	8	ACD28699	cDNA enco	614	14.2	Aab54585 Human LIM	
C 543	14.2	71.0	2347	1	ACD28699	cDNA enco	615	14.2	Aad41265 Human ade	
C 544	14.2	71.0	2362	9	ADB36925	c	616	14.2	Aad41265 Human ade	
C 545	14.2	71.0	2370	7	ACF73789	c	617	14.2	Aad41265 Human ade	
C 546	14.2	71.0	2373	6	ABZ35634	c	618	14.2	Aad41265 Human ade	
C 547	14.2	71.0	2373	6	ABZ35634	cDNA enco	619	14.2	Aad41265 Human ade	
C 548	14.2	71.0	2373	6	ABN95867	c	620	14.2	Aab54585 Human LIM	
C 549	14.2	71.0	2429	8	ACM03893	c	621	14.2	Aad41265 Human ade	
C 550	14.2	71.0	2429	8	ACM03893	cDNA enco	622	14.2	Aad41265 Human ade	
C 551	14.2	71.0	2437	4	ADM16311	c	623	14.2	Aad41265 Human ade	
C 552	14.2	71.0	2451	2	AQ04235	c	624	14.2	Aad41265 Human ade	
C 553	14.2	71.0	2456	7	AD54586	c	625	14.2	Aad41265 Human ade	
C 554	14.2	71.0	2468	5	ADG69788	c	626	14.2	Aad41265 Human ade	
C 555	14.2	71.0	2485	6	ADG69788	cDNA enco	627	14.2	Aad41265 Human ade	
C 556	14.2	71.0	2485	9	ADB53859	c	628	14.2	Aad41265 Human ade	
C 557	14.2	71.0	2487	4	ADM45126	c	629	14.2	Aad41265 Human ade	
C 558	14.2	71.0	2549	2	ADM67219	c	630	14.2	Aad41265 Human ade	
C 559	14.2	71.0	2562	5	ADM60602	c	631	14.2	Aad41265 Human ade	
C 560	14.2	71.0	2570	3	ACD76054	c	632	14.2	Aad41265 Human ade	
C 561	14.2	71.0	2658	5	ABV23126	c	633	14.2	Aad41265 Human ade	
C 562	14.2	71.0	2658	5	ABV23126	cDNA enco	634	14.2	Aad41265 Human ade	
C 563	14.2	71.0	2679	8	ADM37187	c	635	14.2	Aad41265 Human ade	
C 564	14.2	71.0	2684	9	ADM8429	c	636	14.2	Aad41265 Human ade	
C 565	14.2	71.0	2706	6	ADM93089	c	637	14.2	Aad41265 Human ade	
C 566	14.2	71.0	2716	4	ADM22886	c	638	14.2	Aad41265 Human ade	
C 567	14.2	71.0	2718	9	ACD14279	c	639	14.2	Aad41265 Human ade	
C 568	14.2	71.0	2751	7	ABZ59766	c	640	14.2	Aad41265 Human ade	
C 569	14.2	71.0	2751	8	ADM37187	c	641	14.2	Aad41265 Human ade	
C 570	14.2	71.0	2751	8	ADM51726	c	642	14.2	Aad41265 Human ade	
C 571	14.2	71.0	2767	4	ABD12876	c	643	14.2	Aad41265 Human ade	
C 572	14.2	71.0	2771	7	ADM24840	c	644	14.2	Aad41265 Human ade	
C 573	14.2	71.0	2782	4	ADM25495	c	645	14.2	Aad41265 Human ade	
C 574	14.2	71.0	2816	4	ADM15186	c	646	14.2	Aad41265 Human ade	
C 575	14.2	71.0	2824	4	ADM03750	c	647	14.2	Aad41265 Human ade	
C 576	14.2	71.0	2834	9	ADM7105	c	648	14.2	Aad41265 Human ade	
C 577	14.2	71.0	2834	6	ADM61974	c	649	14.2	Aad41265 Human ade	
C 578	14.2	71.0	2834	6	ADM664976	c	650	14.2	Aad41265 Human ade	
C 579	14.2	71.0	2834	6	ADM664976	cDNA enco	651	14.2	Aad41265 Human ade	
C 580	14.2	71.0	2834	6	ADM65641	c	652	14.2	Aad41265 Human ade	
C 581	14.2	71.0	2834	9	ADM92203	c	653	14.2	Aad41265 Human ade	
C 582	14.2	71.0	2834	7	ADM7105	c	654	14.2	Aad41265 Human ade	
C 583	14.2	71.0	2841	7	ADM17933	c	655	14.2	Aad41265 Human ade	
C 584	14.2	71.0	2852	7	ADM53545	c	656	14.2	Aad41265 Human ade	
C 585	14.2	71.0	2867	8	ADM03950	c	657	14.2	Aad41265 Human ade	
C 586	14.2	71.0	2981	6	ADM04186	c	658	14.2	Aad41265 Human ade	
C 587	14.2	71.0	3043	6	ADM35923	c	659	14.2	Aad41265 Human ade	
C 588	14.2	71.0	3043	7	ADM5624	c	660	14.2	Aad41265 Human ade	
C 589	14.2	71.0	3044	3	ADM15166	c	661	14.2	Aad41265 Human ade	
C 590	14.2	71.0	3044	7	ADM95200	c	662	14.2	Aad41265 Human ade	
C 591	14.2	71.0	3044	9	ADM18104	c	663	14.2	Aad41265 Human ade	
C 592	14.2	71.0	3135	4	ADM5194	c	664	14.2	Aad41265 Human ade	
C 593	14.2	71.0	3157	4	ADM22476	c	665	14.2	Aad41265 Human ade	
C 594	14.2	71.0	3169	8	ADM10935	c	666	14.2	Aad41265 Human ade	
C 595	14.2	71.0	3181	6	ADM35925	c	667	14.2	Aad41265 Human ade	
C 596	14.2	71.0	3181	7	ADM56226	c	668	14.2	Aad41265 Human ade	
C 597	14.2	71.0	3199	4	ADM91323	c	669	14.2	Aad41265 Human ade	
C 598	14.2	71.0	3196	9	ADM59152	c	670	14.2	Aad41265 Human ade	
C 599	14.2	71.0	3198	8	ADM39241	c	671	14.2	Aad41265 Human ade	
C 600	14.2	71.0	3198	8	ADM39240	c	672	14.2	Aad41265 Human ade	
C 601	14.2	71.0	3198	8	ADM39243	c	673	14.2	Aad41265 Human ade	
C 602	14.2	71.0	3198	8	ADM39242	c	674	14.2	Aad41265 Human ade	
C 603	14.2	71.0	3199	4	ADM09217	c	675	14.2	Aad41265 Human ade	
C 604	14.2	71.0	3204	9	ADM12570	c	676	14.2	Aad41265 Human ade	
C 605	14.2	71.0	3204	9	ADM59770	c	677	14.2	Aad41265 Human ade	
C 606	14.2	71.0	3207	6	ADM58494	c	678	14.2	Aad41265 Human ade	
C 607	14.2	71.0	3207	6	ADM58494	c	679	14.2	Aad41265 Human ade	
C 608	14.2	71.0	3222	4	ABR02992	c	680	14.2	Aad41265 Human ade	
C 609	14.2	71.0	3243	6	ABR42411	c	681	14.2	Aad41265 Human ade	
C 610	14.2	71.0	3262	9	ABR77694	c	682	14.2	Aad41265 Human ade	
C 611	14.2	71.0	3265	3	ABR26505	c	683	14.2	Aad41265 Human ade	
C 612	14.2	71.0	3265	4	ABR4053	c	684	14.2	Aad41265 Human ade	
C 613	14.2	71.0	3265	4	ABR92092	c	685	14.2	Aad41265 Human ade	
C 614	14.2	71.0	3265	4	ABR42411	c	686	14.2	Aad41265 Human ade	
C 615	14.2	71.0	3265	5	ABR47412	c	687	14.2	Aad41265 Human ade	
C 616	14.2	71.0	3265	6	ABR78656	c	688	14.2	Aad41265 Human ade	
C 617	14.2	71.0	3265	7	ABX77953	c	689	14.2	Aad41265 Human ade	
C 618	14.2	71.0	3265	7	ABX80365	c	690	14.2	Aad41265 Human ade	
C 619	14.2	71.0	3265	7	ACB87022	c	691	14.2	Aad41265 Human ade	
C 620	14.2	71.0	3265	7	ACB87022	cDNA enco	692	14.2	Aad41265 Human ade	
C 621	14.2	71.0	3265	7	ACB87022	cDNA enco	693	14.2	Aad41265 Human ade	
C 622	14.2	71.0	3265	7	ACB87022	cDNA enco	694	14.2	Aad41265 Human ade	
C 623	14.2	71.0	3265	7	ACB87022	cDNA enco	695	14.2	Aad41265 Human ade	
C 624	14.2	71.0	3265	7	ACB87022	cDNA enco	696	14.2	Aad41265 Human ade	
C 625	14.2	71.0	3265	7	ACB87022	cDNA enco	697	14.2	Aad41265 Human ade	
C 626	14.2	71.0	3265	7	ACB87022	cDNA enco	698	14.2	Aad41265 Human ade	
C 627	14.2	71.0	3265	7	ACB87022	cDNA enco	699	14.2	Aad41265 Human ade	
C 628	14.2	71.0	3265	7	ACB87022	cDNA enco	700	14.2	Aad41265 Human ade	
C 629	14.2	71.0	3265	7	ACB87022	cDNA enco	701	14.2	Aad41265 Human ade	
C 630	14.2	71.0	3265	7	ACB87022	cDNA enco	702	14.2	Aad41265 Human ade	
C 631	14.2	71.0	3265	7	ACB87022	cDNA enco	703	14.2	Aad41265 Human ade	
C 632	14.2	71.0	3265	7	ACB87022	cDNA enco	704	14.2	Aad41265 Human ade	
C 633	14.2	71.0	3265	7	ACB87022	cDNA enco	705	14.2	Aad41265 Human ade	
C 634	14.2	71.0	3265	7	ACB87022	cDNA enco	706	14.2	Aad41265 Human ade	
C 635	14.2	71.0	3265	7	ACB87022	cDNA enco	707	14.2	Aad41265 Human ade	
C 636	14.2	71.0	3265	7	ACB87022	cDNA enco	708	14.2	Aad41265 Human ade	
C 637	14.2	71.0	3265	7	ACB87022	cDNA enco	709	14.2	Aad41265 Human ade	
C 638	14.2	71.0	3265	7	ACB87022	cDNA enco	710	14.2	Aad41265 Human ade	
C 639	14.2	71.0	3265	7	ACB87022	cDNA enco	711	14.2	Aad41265 Human ade	
C 640	14.2	71.0	3265	7	ACB87022	cDNA enco	712	14.2	Aad41265 Human ade	
C 641	14.2	71.0	3265	7	ACB87022	cDNA enco	713	14.2	Aad41265 Human ade	
C 642	14.2	71.0	3265	7	ACB87022	cDNA enco	714	14.2	Aad41265 Human ade	
C 643	14.2	71.0	3265	7	ACB87022	cDNA enco	715	14.2	Aad41265 Human ade	
C 644	14.2	71.0	3265	7	ACB87022	cDNA enco	716	14.2	Aad41265 Human ade	
C 645	14.2	71.0	3265	7	ACB87022	cDNA enco	717	14.2	Aad41265 Human ade	
C 646	14.2	71.0	3265	7	ACB87022	cDNA enco	718	14.2	Aad41265 Human ade	
C 647	14.2	71.0	3265	7	ACB87022	cDNA enco	719	14.2	Aad41265 Human ade	
C 648	14.2	71.0	3265	7	ACB87022	cDNA enco	720	14.2	Aad41265 Human ade	
C 649	14.2	71.0	3265	7	ACB87022	cDNA enco	721	14.2	Aad41265 Human ade	
C 650	14.2	71.0	3265	7	ACB87022	cDNA enco	722	14.2	Aad41265 Human ade	
C 651	14.2	71.0	3265	7	ACB87022	cDNA enco	723			



FT /note= "Phosphorothioate backbone"

PT polypeptide, antibody specific to polypeptide or T cell expressing

PT polypeptide.

PN WO200174346-A2.

XX

PD 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010800.

PR 03-APR-2000; 2000US-0194343P.

XX (HYBR-) HYBRIDON INC.

PA

XX

PI Agrawal S, Kandimalla ER, Bregman DB, Mani S, Lu Y;

XX WPI; 2001-662947/76.

PT Increasing sensitivity of cancer cells to a cytotoxin or oxidizing agent

PT useful for therapy comprises contacting them with oligonucleotides

PT complementary to transcription coupled repair or nucleotide excision

PT repair genes.

XX

PS Claim 12; Page 18; 58pp; English.

CC The present invention relates to a method for potentiating or enhancing

CC the toxic effect of a cytotoxin or oxidising agent on a cancer cell,

CC comprising contacting the cell with an oligonucleotide complementary to a

CC gene involved in transcription coupled repair (TCR) and nucleotide

CC excision repair (NER) and with a cytotoxin or oxidising agent. The

CC invention is used to sensitize cancer cells to therapeutic agents. The

CC present sequence is an antisense oligonucleotide directed against

CC Xeroderma pigmentosum group A (XPA) gene

XX

SQ Sequence 20 BP; 4 A; 4 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCATACTATGTTGATG 20

Db 1 GGTCCATACTATGTTGATG 20

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RESULT 2

ABL84566

ID ABL84566 standard; cDNA; 486 BP.

XX

AC ABL84566;

XX

DT 17-MAY-2002 (first entry)

XX

DE Human ovarian cancer related cDNA clone SEQ ID NO:7544.

XX

KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss-

OS Homo sapiens.

XX

PN WO200192581-A2.

XX

PD 06-DEC-2001.

XX

PP 29-MAY-2001; 2001WO-US017756.

XX

PR 26-MAY-2000; 2000US-0207484P.

XX

PA (CORT-) CORIXA CORP.

XX

PT Algate PA, Harlocker SL, Jones R;

XX WPI; 2002-122075/16.

XX

PT Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

XX

PS Claim 1; SEQ ID NO 2117; 48pp; English.

CC The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (III) of a ovarian tumour

CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)

CC from the 10912 nucleotide sequences a given in AB177023 to AB167934,

CC (III) encoding (II) having a sequence (S2), a T cell population of (II),

CC or antigen presenting cells that express (III). (I) has cytostatic

CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for

CC detecting ovarian cancer in a patient's biological sample preferably

CC serum or ovarian tissue. The method comprises contacting a biological

CC sample from a patient with (IV), detecting the amount of polynucleotide

CC hybridising to (IV) and comparing the amount to a predetermined cutoff

CC value and thereby detecting ovarian cancer in the patient, where the

CC amount of polynucleotide hybridising to (IV) is detected preferably by

CC polymerase chain reaction (PCR). (II) comprising (III) and/or (II) is

CC useful for stimulating and/or expanding T cells specific for an ovarian

CC tumour protein comprising contacting T cells with (III) or (II) or (III) is

CC useful in design and preparation of ribozyme molecules for inhibiting

CC expression of the tumour polypeptides and proteins in tumour cells; and

CC to isolate a full length gene from a suitable library e.g., a tumour cDNA

XX library using well known techniques

SQ Sequence 486 BP; 121 A; 106 C; 70 G; 188 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 6; Length 486;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCATACTATGTTGATG 20

Db 149 GGTCCATACTATGTTGATG 168

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RESULT 3

ABL79139/C

ID ABL79139 standard; cDNA; 506 BP.

XX

AC ABL79139;

XX

DT 17-MAY-2002 (first entry)

XX

DE Human ovarian cancer related cDNA clone SEQ ID NO:2117.

XX

Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss-

OS Homo sapiens.

XX

PN WO200192581-A2.

XX

PD 06-DEC-2001.

XX

PP 29-MAY-2001; 2001WO-US017756.

XX

PR 26-MAY-2000; 2000US-0207484P.

XX

PA (CORT-) CORIXA CORP.

XX

PT Algate PA, Harlocker SL, Jones R;

XX WPI; 2002-122075/16.

XX

PT Composition for therapy and diagnosis of ovarian cancer comprising

PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding

PT polypeptide, antibody specific to polypeptide or T cell expressing

XX

PS Claim 1; SEQ ID NO 2117; 48pp; English.

CC The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of a ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)  
 CC from the 10912 nucleotide sequences as given in ABL77023 to ABL7934,  
 CC (III) encoding (II) having a sequence (S2), a T cell population of (II),  
 CC or antigen presenting cells that expresses (II). (II) has cytotoxic  
 CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for  
 CC detecting ovarian cancer in a patient's biological sample preferably  
 CC serum or ovarian tissue. The method comprises contacting a biological  
 CC sample from a patient with (IV), detecting the amount of polynucleotide  
 CC hybridising to (IV) and comparing the amount to a predetermined cutoff  
 CC value and thereby detecting ovarian cancer in the patient, where the  
 CC amount of polynucleotide hybridising to (IV) is detected preferably by  
 CC polymerase chain reaction (PCR). (II) comprising (III) and/or (II) is  
 CC useful for stimulating and/or expanding T cells specific for an ovarian  
 CC tumour protein comprising contracting T cells with (III) or (II). (III) is  
 CC useful in design and preparation of ribozyme molecules for inhibiting  
 CC expression of the tumour polypeptides and proteins in tumour cells; and  
 CC to isolate a full length gene from a suitable library e.g., a tumour cDNA  
 CC library using well known techniques

XX SQ Sequence 506 BP; 174 A; 95 C; 104 G; 132 T; 0 U; 1 Other;  
 Best Local Similarity 100.0%; Pred. No. 3.6; Mismatches 20;  
 Matches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 GGTCCATACTCATGTTGATG 20  
 Db 246 GGTCGATACATCTAGTGTGATG 227

RESULT 4  
 ABL79129  
 ID ABL79129 standard; cDNA; 513 BP.  
 XX AC ABL79129;  
 XX DT 17-MAY-2002 (first entry)  
 XX DE Human ovarian cancer related cDNA clone SEQ ID NO:2107.  
 KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO200192581-A2.  
 XX PD 06-DEC-2001.  
 XX PF 29-MAY-2001; 2001WO-US017756.  
 XX PR 26-MAY-2000; 2000US-0207484P.  
 XX PA (CORI-) CORTEX CORP.  
 XX PI Algate PA, Harlocker SL, Jones R;  
 XX DR WPI; 2002-122075/16.

PT Composition for therapy and diagnosis of ovarian cancer comprising  
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding  
 PT polypeptide, antibody specific to polypeptide or T cell expressing  
 PT polypeptide.

PS Claim 1; SEQ ID NO 2107; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers  
 CC and immunosimulants; and a polypeptide (II) of a ovarian tumour  
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)  
 CC from the 10912 nucleotide sequences as given in ABL77023 to ABL7934,  
 CC (III) encoding (II) having a sequence (S2), a T cell population of (II),  
 CC or antigen presenting cells that expresses (II). (II) has cytotoxic  
 CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for  
 CC detecting ovarian cancer in a patient's biological sample preferably  
 CC serum or ovarian tissue. The method comprises contacting a biological  
 CC sample from a patient with (IV), detecting the amount of polynucleotide  
 CC hybridising to (IV) and comparing the amount to a predetermined cutoff  
 CC value and thereby detecting ovarian cancer in the patient, where the  
 CC amount of polynucleotide hybridising to (IV) is detected preferably by  
 CC polymerase chain reaction (PCR). (II) comprising (III) and/or (II) is  
 CC useful for stimulating and/or expanding T cells specific for an ovarian  
 CC tumour protein comprising contracting T cells with (III) or (II). (III) is  
 CC useful in design and preparation of ribozyme molecules for inhibiting  
 CC expression of the tumour polypeptide and proteins in tumour cells; and  
 CC to isolate a full length gene from a suitable library e.g., a tumour cDNA  
 CC library using well known techniques

XX SQ Sequence 513 BP; 144 A; 95 C; 100 G; 166 T; 0 U; 8 Other;  
 Best Local Similarity 100.0%; Pred. No. 3.7; Mismatches 20;  
 Matches 20; Conservative 0; Indels 0; Gaps 0;

QY 1 GGTCCATACTCATGTTGATG 20  
 Db 357 GGTCGATACATCTAGTGTGATG 376

RESULT 5  
 AAS63227/C  
 ID AAS63227 standard; cDNA; 822 BP.  
 XX AC AAS63227;  
 XX DT 29-JAN-2002 (first entry)  
 XX DE Human xeroderma pigmentosum complementation group A (XPA) DNA.  
 XX DN DNA mutation-binding protein; nuclease; DNA mismatch; cancer; PCR primer;  
 KW DNA damage; human xeroderma pigmentosum complementation group; XPF; XPA;  
 KW XPC; XPE; ERCCA; human MutS homologue 2; hush2; MutS; Nuc; MutY; Fpg; ss;  
 KW Fapy-DNA glycosylase; uracil DNA glycosylase; ung; TDG; xthu; gene; Uvr A;  
 KW A/G-specific adenosine glycosylase; synthetic T4 endonuclease V; T4 endo V;  
 KW thymine DNA-glycosylase; Uvr B; Uvr C; nth gene; nfo gene; exonuclease;  
 KW endonuclease.  
 XX OS Homo sapiens.  
 XX PN WO200173079-A2.  
 XX PD 04-OCT-2001.  
 XX PF 26-MAR-2001; 2001WO-US009700.  
 XX PR 28-MAR-2000; 2000US-0192764P.  
 XX PR 29-AUG-2000; 2000US-00650855.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Mc Cutchen- Maloney SL;  
 XX DR WPI; 2001-656920/75.  
 XX P-PSDB; AAU69740.

PT Recombinant chimeric protein, useful for detecting and quantifying DNA  
 PT mutations, e.g. in disease diagnosis, comprises mutation-binding protein  
 PT and nuclease.

PS Claim 46; Page 62; 128pp; English.

XX Sequences AAS63224-AAS63305 represent cDNA encoding and PCR primers used  
 CC to amplify cDNA encoding protein which can be used in the synthesis of  
 CC chimeric proteins comprising a DNA mutation-binding protein, a linker and  
 CC a nuclease, by recombinant technology. The chimeric proteins are useful  
 CC for detection, quantification and mapping of DNA sequence variations  
 CC including mutations, for example, caused by damage and mismatches. The

CC proteins are able to bind to the site of the DNA mutation and cut it out of the molecule. This is useful for early diagnosis of cancer and other diseases. The proteins used in the invention include human XPF (or ERCC4), human xeroderma pigmentosum complementation groups A, C and B (XPA, XPC and XPE), human MutS homologue 2 (hMSH2), Serrata marcescens nuclease (Nuc), Thermus thermophilus MutS, Escherichia coli Fapy-DNA-glycosylase (Fpg), uracil DNA glycosylase (ung), A/G-specific adenine glycosylase (MutY), synthetic T4 endonuclease V (T4 endo V), thymine DNA-glycosylase (TDG), E. coli Uvr A, B and C, and E. coli endonucleases and exonucleases.

SQ Sequence 822 BP; 280 A; 144 C; 225 G; 173 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 822;  
Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTCCATACTCAGTTGATG 20  
Db 743 GGTCATACATGTTGATG 724

RESULT 6

AAD21394/c  
ID AAD21394 standard; DNA; 1377 BP.  
XX  
AC  
XX  
DT 28-JAN-2002 (first entry)  
XX  
DB Human Xeroderma pigmentosum group A (XPA) DNA.  
XX  
KW Human; cytotoxin; cancer; transcription coupled repair; TCR;  
nucleotide excision repair; NER; cyostatic; chromosome 9;  
Xeroderma pigmentosum group A; XPA; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200174346-A2.  
XX  
PR 11-OCT-2001.  
XX  
PP 03-APR-2001; 2001WO-US010800.  
XX  
PR 03-APR-2000; 2000US-0194343P.  
XX  
PA (HYBR-) HIBRIDON INC.  
XX  
PI Agrawal S, Kandimalla ER, Bregman DB, Mani S, Lu Y;  
XX  
DR WPI; 2001-662947/76.

Increasing sensitivity of cancer cells to a cytotoxin or oxidizing agent complementary to transcription coupled repair or nucleotide excision repair genes.

PS Disclosure; Page 48; 58pp; English.

PT Increasing sensitivity of cancer cells to a cytotoxin or oxidizing agent useful for therapy comprises contacting them with oligonucleotides complementary to transcription coupled repair or nucleotide excision repair genes.

XX The present invention relates to a method for potentiating or enhancing the toxic effect of a cytotoxin or oxidising agent on a cancer cell, comprising contacting the cell with an oligonucleotide complementary to a gene involved in transcription coupled repair (TCR) and nucleotide excision repair (NER) and with a cytotoxin or oxidising agent. The invention is used to sensitize cancer cells to therapeutic agents. The present sequence is a human Xeroderma pigmentosum group A (XPA) gene located on chromosome 9

XX Sequence 1377 BP; 458 A; 232 C; 358 G; 329 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 4.2; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC proteins are able to bind to the site of the DNA mutation and cut it out of the molecule. This is useful for early diagnosis of cancer and other diseases. The proteins used in the invention include human XPF (or ERCC4), human xeroderma pigmentosum complementation groups A, C and B (XPA, XPC and XPE), human MutS homologue 2 (hMSH2), Serrata marcescens nuclease (Nuc), Thermus thermophilus MutS, Escherichia coli Fapy-DNA-glycosylase (Fpg), uracil DNA glycosylase (ung), A/G-specific adenine glycosylase (MutY), synthetic T4 endonuclease V (T4 endo V), thymine DNA-glycosylase (TDG), E. coli Uvr A, B and C, and E. coli endonucleases and exonucleases.

SQ Sequence 822 BP; 280 A; 144 C; 225 G; 173 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 822;  
Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGTCCATACTCAGTTGATG 20  
Db 743 GGTCATACATGTTGATG 724

RESULT 7

AAS34872/c  
ID AAS34872 standard; CDNA; 1407 BP.  
XX  
AC AAS34872;  
XX  
DT 04-DEC-2001 (first entry)  
XX  
CDNA encoding novel human neoplastic disease associated polypeptide #106.  
XX  
Human; neoplastic disease associated polypeptide; cancer; gene therapy; hyperproliferative disorder; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; neuroprotective; cyostatic; anti inflammatory; vasotropic; ss.

XX  
OS Homo sapiens.  
XX  
PN WO2001155163-A1.  
XX  
PR 02-APR-2001.  
XX  
PP 17-JAN-2001; 2001WO-US001358.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0221664P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226868P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 06-SEP-2000; 2000US-0230437P.

PR 06-SEP-2000; 2000US-023043BP.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-023143P.  
 PR 08-SEP-2000; 2000US-0231434P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-02331988P.  
 PR 14-SEP-2000; 2000US-0233297P.  
 PR 14-SEP-2000; 2000US-0233305P.  
 PR 14-SEP-2000; 2000US-02332399P.  
 PR 14-SEP-2000; 2000US-02332400P.  
 PR 14-SEP-2000; 2000US-02342401P.  
 PR 14-SEP-2000; 2000US-0233053P.  
 PR 14-SEP-2000; 2000US-02332964P.  
 PR 14-SEP-2000; 2000US-02334223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234998P.  
 PR 26-SEP-2000; 2000US-0235434P.  
 PR 27-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236337P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 02-OCT-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 20-OCT-2000; 2000US-0240950P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 20-OCT-2000; 2000US-0241826P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-024474P.  
 PR 08-NOV-2000; 2000US-024475P.  
 PR 08-NOV-2000; 2000US-024476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-024652P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.

Query Match 100.0%; Score 20; DB 4; Length 1407;  
 Best Local Similarity 100.0%; Pred. No. 4.2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 GGTCCCATACTCATGTTGATG 20
Db	'782 GGTCCCATACTCATGTTGATG 763

RESULT 8  
 ADC46310/C  
 ID ADC46310 standard; cDNA: 1407 BP.  
 XX  
 AC  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human neoplastic disease-associated gene 106 cDNA #1.  
 XX

KW Neoplastic disease-associated polypeptide; gene therapy;  
 KW hyperproliferative disease; cancer; autoimmune disorder; diabetes;  
 KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;  
 KW autoimmune thyroiditis; haemolytic anaemia; haemopoietic disorder;  
 KW haematologic disorder; anaemia; thrombocytopaenia; allergic reaction;  
 KW asthma; eczema; inflammatory disorder;  
 KW inflammatory bowel disease; Crohn's disease; neurodegenerative disorder;  
 KW Alzheimer's disease; Parkinson's disease; renal disorder;  
 KW acute glomerulonephritis; end-stage renal disease;  
 KW cardiovascular disorder; atherosclerosis; myocarditis;  
 KW infectious disease; AIDS; cachexia; anorexia; wound healing;  
 KW epithelial cell proliferation; Human; ss.  
 XX OS  
 XX Homo sapiens.  
 XX US2003082758-A1.  
 XX PN  
 XX PD 01-MAY-2003.  
 XX XX  
 XX 22-MAR-2002; 2002US-00103313.  
 PR XX  
 PR 31-JAN-2000; 2000US-0179055P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184654P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214866P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0224520P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
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 PR 14-AUG-2000; 2000US-0225275P.  
 PR 14-AUG-2000; 2000US-0225275P.  
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 PR 14-AUG-2000; 2000US-0226688P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-022758P.  
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 PR 05-SEP-2000; 2000US-0229513P.  
 PR 01-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
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 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-02331988P.

PR 14-SEP-2000; 2000US-0233397P.  
 PR 14-SEP-2000; 2000US-0233398P.  
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 PR 14-SEP-2000; 2000US-0233400P.  
 PR 14-SEP-2000; 2000US-0233401P.  
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 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 20-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 20-OCT-2000; 2000US-0241826P.  
 PR 01-NOV-2000; 2000US-0241617P.  
 PR 08-NOV-2000; 2000US-0241785P.  
 PR 08-NOV-2000; 2000US-0241786P.  
 PR 08-NOV-2000; 2000US-0241787P.  
 PR 08-NOV-2000; 2000US-0241808P.  
 PR 08-NOV-2000; 2000US-0241809P.  
 PR 08-NOV-2000; 2000US-0241826P.  
 PR 08-NOV-2000; 2000US-0244647P.  
 PR 08-NOV-2000; 2000US-0245228P.  
 PR 08-NOV-2000; 2000US-0245232P.  
 PR 08-NOV-2000; 2000US-0245244P.  
 PR 08-NOV-2000; 2000US-0245255P.  
 PR 08-NOV-2000; 2000US-0245262P.  
 PR 08-NOV-2000; 2000US-0245267P.  
 PR 08-NOV-2000; 2000US-0245278P.  
 PR 08-NOV-2000; 2000US-0245288P.  
 PR 08-NOV-2000; 2000US-0245622P.  
 PR 08-NOV-2000; 2000US-0245623P.  
 PR 08-NOV-2000; 2000US-0245624P.  
 PR 08-NOV-2000; 2000US-0245610P.  
 PR 08-NOV-2000; 2000US-0245611P.  
 PR 08-NOV-2000; 2000US-0245613P.  
 PR 08-NOV-2000; 2000US-0245614P.  
 PR 17-NOV-2000; 2000US-0245207P.  
 PR 17-NOV-2000; 2000US-0245208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
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 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
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 PR 17-NOV-2000; 2000US-0249219P.  
 PR 17-NOV-2000; 2000US-0249220P.  
 PR 17-NOV-2000; 2000US-0249221P.  
 PR 17-NOV-2000; 2000US-0249222P.  
 PR 17-NOV-2000; 2000US-0249223P.  
 PR 17-NOV-2000; 2000US-0249224P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249246P.  
 PR 17-NOV-2000; 2000US-0249247P.  
 PR 17-NOV-2000; 2000US-0249248P.  
 PR 17-NOV-2000; 2000US-0249249P.  
 PR 17-NOV-2000; 2000US-0249250P.

PR	05-DEC-2000; 2000US-0251030P.	PN	WO200274979-A2.
XX	05-DEC-2000; 2000US-0251989P.	XX	26-SEP-2002.
PD	05-DEC-2000; 2000US-0256719P.	XX	
PR	05-DEC-2000; 2000US-0251479P.	XX	
PR	08-DEC-2000; 2000US-0251856P.	XX	20-MAR-2002; 2002WO-US008456.
PR	08-DEC-2000; 2000US-0251868P.	XX	
PR	08-DEC-2000; 2000US-0251869P.	XX	20-MAR-2002; 2002WO-US008456.
PR	08-DEC-2000; 2000US-0251989P.	XX	
PR	08-DEC-2000; 2000US-0251990P.	XX	(ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
PR	11-DEC-2000; 2000US-0254097P.	XX	
PR	11-JAN-2001; 2001US-0259678P.	XX	WPI; 2003-786918/74.
PR	17-JAN-2001; 2001US-00764854.	XX	P-PSDB; ADC46314.
PA	(HUMA-) HUMAN GENOME SCI INC.	XX	
XX	New isolated human neoplastic disease-associated polypeptides and	PT	
PI	polyNUCLEOTIDES, useful for diagnosing, preventing, Prognosticating or	PT	New gene expression profile generated from primary, endothelial,
Rosen CA, Ruben SM, Barash SC;	treating medical conditions such as cancer, AIDS, diabetes or parkinson's	PT	epithelial, and muscle cell types, useful for identifying disease
XX	disease.	PT	pathologies involving alterations of gene expression, e.g. cancer.
WPI; 2003-786918/74.		XX	
DR	P-PSDB; ADC46314.	XX	
XX	Claim 1; SEQ ID NO 116; 302pp; English.	XX	Disclosure; Page 716-718; 850pp; English.
PS		XX	
XX	The invention relates to one of 238 disclosed human neoplastic disease-associated polypeptides encoded by 171 disclosed cDNA sequences	CC	
CC	(including their domains, epitopes, full-length proteins, allelic variants	CC	genes (AB234899-AB235692) and generated from a cell type. The cell type
CC	or species homologues). Also included are those encoding nucleic acids, a	CC	is a coronary artery endothelium, umbilical artery or vein endothelium,
CC	recombinant vector comprising the nucleic acid, a recombinant host cell	CC	aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC	comprising the nucleic acid (expressing the protein), an isolated	CC	endothelium, myometrium microvascular endothelium, keratinocyte
CC	antibody that binds specifically to the isolated polypeptide, Preventing,	CC	epithelium, bronchial epithelium, mammary epithelium, prostate epithelium,
CC	treating or ameliorating a medical condition, diagnosing a pathological	CC	small airway epithelium, renal proximal tubule epithelium,
CC	condition or a susceptibility to a pathological	CC	muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC	identifying a binding partner to the polypeptide, identifying an activity	CC	dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC	in a biological assay, and the gene corresponding to the cDNA sequence.	CC	aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC	The polypeptides, polynucleotides and antibodies are useful for	CC	bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC	detecting, preventing, diagnosing, prognosticating, treating or	CC	osteoblasts or prostate stromal cell. The gene expression profile is used
CC	ameliorating medical conditions such as hyperproliferative diseases or	CC	for determining the level of RNA expression for a sample, determining the
CC	cancer, autoimmune disorders (e.g. rheumatoid arthritis <sup>B</sup> , systemic lupus erythematosus, multiple sclerosis, autoimmune thyroiditis	CC	phenotype of a cell and distinguishing cell types. The gene or a protein
CC	or haemolytic anaemia), haematopoietic or hematologic disorders (e.g.	CC	expression profile is useful in identifying disease pathologies involving
CC	anaemia or thrombocytopaenia), allergic reactions including asthma or	CC	alterations of gene expression. The assessment of expression profiles may
CC	eczema, inflammatory disorders (e.g. ischaemia-reperfusion injury,	CC	provide meaningful information with respect to tumour type and stage,
CC		CC	treatment methods, and prognosis. The gene or protein expression profile
CC		CC	may also be used for creating microarrays. The microarray is useful for
CC		CC	genetic and physical mapping of genomes, DNA sequencing, genetic or
CC		CC	medical diagnosis, genotyping of organisms, confirming cell or tissue
CC		CC	identifications and in identifying promising antibiotics, antiviral or
CC		CC	antifungal agents
XX	Sequence 4670 BP; 1072 A; 1094 C; 977 G; 1055 T; 0 U; 472 Other;	SQ	
Query Match	100.0%	Score 20;	DB 9;
Best Local Similarity	100.0%	Length 1407;	
Matches 20;	Conservative 0;	Mismatches 0;	
Indels 0;	Gaps 0;		
QY	1 GGTCCATACATCGATGTGATG 20	QY	1 GGTCCATACATCGATGTGATG 20
Db	782 GGTCCATACATCGATGTGATG 763	Db	695 GGTCCATACATCGATGTGATG 714
RESULT 9		RESULT 10	
AB235476	AB235476 standard; cDNA; 4670 BP.	ABX05799	ABX05799
XX		XX	ID ABX05799 standard; DNA; 1029 BP.
AC	AB235476;	AC	
XX		XX	
DT	05-FEB-2003 (first entry)	DT	27-OCT-2003 (revised)
XX		DT	11-FEB-2003 (first entry)
DE	Human gene expression profile polynucleotide SEQ ID NO 587.	XX	S. pneumoniae type 4 strain coding region #87.
XX		XX	
KW	Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;	XX	
KW	bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;	XX	
KW	tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;	XX	
KW	gene expression; gene; ss.	XX	Gene; ds; bacterial meningitis; pneumonia; sepsis; otitis media;
OS	Homo sapiens.	XX	ear infection; antiinflammatory; antibacterial; immunostimulant;
OS		XX	auditory; respiratory; gene therapy; vaccine.
OS		XX	Streptococcus pneumoniae; type 4 strain.
XX		XX	

PN WO200277021-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 KW  
 PF 27-MAR-2002; 2002WO-1B002163.  
 XX  
 DR 27-MAR-2001; 2001GB-00007658.  
 XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX  
 PT Massignani V, Tettelin H, Fraser C;  
 XX  
 DR WPI; 2003-040579/03.  
 DR P-PSDB; ABU0520.  
 XX  
 PT New proteins and nucleic acid molecules from *Streptococcus pneumoniae*,  
 PT useful as medicaments for treating or preventing a disease or infection,  
 PT due to *streptococcus* bacteria, such as pneumonia, sepsis, otitis media or  
 PT ear infection.  
 PS Claim 6; SEQ ID NO 173; 56pp; English.  
 XX  
 CC The invention relates to a protein comprising or having at least 50%  
 CC identity to any of the 2469 amino acid sequences, identified in the  
 CC specification (available on a computer readable format), or its fragment,  
 CC expressed from 2469 of 2489 identified DNA coding regions from the  
 CC *Streptococcus pneumoniae* type 4 strain genomic sequence appearing as  
 CC ABS56454. Also included are an antibody which binds one of the proteins,  
 CC treating a patient by administering the protein, DNA or antibody (in a  
 CC composition), a kit comprising first and second primers, which are the  
 CC nucleic acid cited above or fragments between nucleotides 8-100 of a  
 CC sequence not defined in the specification, for amplifying a target  
 CC sequence contained within a *Streptococcus* nucleic acid sequence, where  
 CC the first primer is substantially complementary to the target sequence  
 CC and the second primer is substantially complementary to the complement of  
 CC the target sequence, and where the parts of the primers having  
 CC substantial complementarity define the termini of the target sequence to  
 CC be amplified, assay comprising contacting a test compound with the  
 CC protein, and determining whether the test compound binds to the protein  
 CC and a *Streptococcus pneumoniae* bacterium, where one or more genes  
 CC encoding the proteins have been rendered inactive. The proteins, nucleic  
 CC acid molecules, antibody and compositions are useful as medicaments for  
 CC treating or preventing a disease or infection due to *streptococcus*  
 CC bacteria, particularly *S. pneumoniae*, such as pneumonia, sepsis, otitis  
 CC media or ear infection. They are also useful in developing vaccines,  
 CC diagnostics and antibiotics. The methods are useful for identifying  
 CC immunodominant proteins. The present sequence is one of the 2489  
 CC identified coding region from the genomic sequence. Note: The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from WIPO at  
 CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences). (Updated on 27-OCT-2003 to  
 CC standardise OS field)  
 SQ Sequence 1029 BP; 305 A; 221 C; 212 G; 291 T; 0 U; 0 Other;  
 Query Match 84.0%; Score 16.8; DB 7; Length 1029;  
 Best Local Similarity 90.0%; Pred. No. 1.6e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GGTCCATACTCATGTGATG 20  
 Db 975 GGTCCATGCTCATGTAGATG 994  
 RESULT 11  
 AAV52173/C  
 ID AAV52173 standard; DNA; 14273 BP.  
 AC AAV52173;  
 XX  
 DT 23-OCT-1998 (first entry)  
 XX

---

DE Streptococcus pneumoniae genome fragment SEQ ID NO:40.  
 XX  
 KW Streptococcus pneumoniae; *S. pneumoniae*; genome; diagnosis; assay;  
 KW computer readable medium; vaccine; pharmaceutical composition; ds.  
 KW  
 OS Streptococcus pneumoniae.  
 XX  
 PN WO9818931-A2.  
 XX  
 PD 07-MAY-1998.  
 XX  
 PT 30-OCT-1997; 97WO-US019588.  
 XX  
 PR 31-OCT-1996; 96US-0029960P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PT Kunsch CA, Choi GH, Dillon PJ, Rosen CA, Barash SC, Fannon M;  
 PI Dougherty BA;  
 XX  
 PT Computer-readable medium with recorded *Streptococcus pneumoniae*  
 PT polynucleotide sequences - useful in diagnostic kits and assays, and  
 pharmaceutical compositions and vaccines for *Streptococcus pneumoniae*.  
 XX  
 PT  
 CC The present invention describes a computer readable medium which has the  
 CC nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded  
 CC on it, or a representative fragment or a sequence at least 95% identical  
 CC to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1  
 CC to 391 (AAV52134 to AAV52524) are genomic fragments from *Streptococcus*  
 CC pneumoniae. The present invention also describes an isolated nucleic acid  
 CC molecule encoding a homologue of any of the fragments of the *S.pneumoniae*  
 CC genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced  
 CC by a process comprising: (a) screening a genomic DNA library using as a  
 CC probe a target sequence defined by any of the sequences in SEQ ID NO:1 to  
 CC 391, identifying members of the library which contain sequences that  
 CC hybridise to the target sequence and isolating the nucleic acid molecules  
 CC from the members; or (b) isolating mRNA, DNA or cDNA produced from an  
 CC organism, amplifying nucleic acids whose nucleotide sequence is  
 CC homologous to amplification primers derived from the fragment of the *S.*  
 CC *pneumoniae* genome to prime the amplification and isolating the amplified  
 CC sequences. The computer readable medium can be used in a computer-based  
 CC system for identifying fragments of the *S. pneumoniae* genome of  
 CC commercial importance, or expression modulating fragments of the *S.*  
 CC *pneumoniae* genome. Products from the present invention can be used in  
 CC diagnosis kits and assays, and pharmaceutical compositions and vaccines  
 CC for *S. pneumoniae*.  
 XX  
 SQ Sequence 14273 BP; 4357 A; 2428 C; 2694 G; 4794 T; 0 U; 0 Other;  
 Query Match 84.0%; Score 16.8; DB 2; Length 14273;  
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GGTCCATACTCATGTGATG 20  
 Db 13385 GGTCCATGCTCATGTAGATG 13366  
 RESULT 12  
 ABS56454\_00/C  
 ABS56454\_00/C sequence split into 22 fragments LOCUS ABS56454 Accession Abs56454  
 WP Fragment Name Begin End  
 WP ABS56454\_00 11000 21000  
 WP ABS56454\_01 10001 21000  
 WP ABS56454\_02 20001 31000  
 WP ABS56454\_03 30001 41000  
 WP ABS56454\_04 40001 51000  
 WP ABS56454\_05 50001 61000  
 WP ABS56454\_06 60001 71000

WP ABS56454\_07 70001 81000  
 WP ABS56454\_08 80001 91000  
 CC ABS56454\_09 90001 101000  
 CC ABS56454\_10 100001 110000  
 CC ABS56454\_11 110000 121000  
 CC ABS56454\_12 120000 131000  
 WP ABS56454\_13 130001 141000  
 WP ABS56454\_14 140000 151000  
 WP ABS56454\_15 150000 161000  
 WP ABS56454\_16 160000 171000  
 WP ABS56454\_17 170000 181000  
 WP ABS56454\_18 180000 191000  
 WP ABS56454\_19 190000 201000  
 WP ABS56454\_20 200000 211000  
 ID ABS56454 Standard; DNA; 2162598 BP.  
 AC ABS56454;  
 XX DT 27-OCT-2003 (revised)  
 DT 10-FEB-2003 (first entry)  
 XX DE Streptococcus pneumoniae type 4 strain complete genome.  
 KW ds; bacterial meningitis; pneumonia; sepsis; otitis media; genome;  
 KW ear infection; antiinflammatory; antibacterial; immunostimulant;  
 KW auditory; respiratory; gene therapy; vaccine.  
 OS Streptococcus pneumoniae; type 4 strain.  
 PN WO200277021-A2.  
 XX PD 03-OCT-2002.  
 XX PR 27-MAR-2002; 2002WO-IB002163.  
 XX PR 27-MAR-2001; 2001GB-00007658.  
 XX PR (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX PI Masignani V, Tettelin H, Fraser C;  
 XX DR WPI; 2003-040579/03.  
 XX PT New proteins and nucleic acid molecules from *Streptococcus pneumoniae*, useful as medicaments for treating or preventing a disease or infection due to *streptococcus* bacteria, such as pneumonia, sepsis, otitis media or ear infection.  
 PT Claim 17; SBQ ID NO 4979; 56pp; English.  
 XX The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the *Streptococcus pneumoniae* type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a target sequence contained within a *Streptococcus* nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantial complementarity define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein and determining whether the test compound binds to the protein and a *Streptococcus pneumoniae* bacterium where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to *streptococcus*

CC bacteria, particularly *S. pneumoniae*, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant protein. The present sequence is the *Streptococcus pneumoniae* type 4 strain genome sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published\_pct\_sequences. (Updated on 27-OCT-2003 to standardise OS field)

XX Sequence 2162598 BP; 654373A; 427176C; 431369G; 649680T; 0U; 0other; Query Match 84.0%; Score 16.8; DB 7; Length 110000; Best Local Similarity 90.0%; Fred. No. 3.1e+02; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0; OY 1 GGTCCATCACTCATGTGATG 20  
 Db 67573 GGTCAGCTCATGTAGATG 67554

RESULT 13  
 ABT1396/c  
 ID ABT1396 standard; DNA; 6765 BP.

XX ABT1396;  
 AC 13-FEB-2003 (first entry)

XX DE Human Cryptovirus strain BBR DNA region SEQ ID No 23.  
 XX Neuroprotective; virucide; anticonvulsant; antiinflammatory; Cryptovirus;  
 KW idopathic; neurological; neurodegenerative; neuropsychological; vaccine;  
 KW epilepsy; neuropsychiatric disorder; subacute sclerosing panencephalitis;  
 KW epileptiform disease; multiple sclerosis; chronic fatigue syndrome;  
 KW primary lymphadenopathy-associated illness; gene therapy; dB.  
 XX OS Rubulavirus sp.  
 XX PN WO200277211-A2.  
 XX PD 03-OCT-2002.  
 XX PP 07-FEB-2002; 2002WO-US004117.  
 XX PR 07-FEB-2001; 2001US-0267253P.  
 XX PA (CRYP-) CRYPTIC AFFLICTIONS LLC.  
 XX PI Robbins SJ;  
 XX DR WPI; 2003-040586/03.  
 XX P-PSDB; ABU18512.

PT New nucleic acid useful for diagnosing and treating idiopathic neurological disorders, including epilepsy, multiple sclerosis, and lymphadenopathy-associated illnesses, and in screening of potential new antiviral drugs.

XX Disclosure; Page 228-235; 262pp; English.

XX The invention relates to an isolated nucleic acid comprising: contiguous nucleotide positions 1-15246 of a sequence comprising 15246 bp fully defined in the specification; a nucleic acid sequence complementary to the 15246bp sequence; or a Cryptovirus-specific fragment of the 15246bp or its complement, at least about 5 nucleotides long. The nucleic acid is useful in diagnosing and treating many idopathic neurological, neurodegenerative, neuropsychological and neuropsychiatric disorders, including epilepsy, multiple sclerosis, chronic fatigue syndrome or subacute sclerosing panencephalitis) and primary lymphadenopathy-associated illnesses, and in research and development, including screening of potential new antiviral drugs. The nucleic acid, protein and the viral particle are useful in manufacturing

CC a vaccine. The protein is also used in producing a Cryptovirus-specific antibody. The antibody may also be used in manufacturing a medicament for the treatment of Cryptovirus infections. The polynucleotides of the invention can be used to treat disorders by gene therapy. This

CC polynucleotide sequence represents a DNA region of the human Cryptovirus

XX strain BBR of the invention

SQ Sequence 6765 BP; 2139 A; 1351 C; 1357 G; 1918 T; 0 U; 0 Other;

Query Match 82.0%; Score 16.4; DB 7; Length 6765;

Best Local Similarity 94.4%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATACTCATGTTGATG 20

Db 4712 TCCATACTCATGTTGATG 4695

RESULT 14

ABT13954/C

ID ABT13954 standard; DNA; 15246 BP.

XX

AC ABT13954;

XX

DT 13-FEB-2003 (first entry)

XX Human Cryptovirus strain BBR coding sequence SEQ ID No 1.

XX Neuroprotective; virucide; anticonvulsant; antiinflammatory; Cryptovirus; idopathic; neurological; neurodegenerative; neuropsychological; vaccine; epilepsy; neuropsychiatric disorder; Subacute sclerosing panencephalitis; epileptiform disease; multiple sclerosis; chronic fatigue syndrome; primary lymphadenopathy-associated illness; gene therapy; gene; ds.

OS Rubulavirus sp.

XX

PN WO200277211-A2.

XX

PA 03-OCT-2002.

PD

XX

PP 07-FEB-2002; 2002WO-US004117.

XX

PR 07-FEB-2001; 2001US-0267253P.

XX

PA (CRYP-) CRYPTIC AFFLICTIONS LLC.

XX

PT Robbins SJ;

XX

DR WPI; 2003-040586/03.

XX

PT New nucleic acid useful for diagnosing and treating idiopathic neurological disorders, including epileptiform diseases, e.g. epilepsy, and lymphadenopathy-associated illnesses, and in screening of potential new antiviral drugs.

XX

PS Claim 1; Fig 9; 262PP; English.

XX

The invention relates to an isolated nucleic acid comprising: contiguous nucleotide positions 1-15446 of a sequence comprising 15246 bp fully defined in the specification; a nucleotide sequence complementary to the 15246bp sequence; or a Cryptovirus-specific fragment of the 15246bp or its complement, at least about 5 nucleotides long. The nucleic acid is useful in diagnosing and treating many idiopathic neurological, neurodegenerative, neuropsychological and neuropsychiatric disorders, including epileptiform diseases (e.g. epilepsy, multiple sclerosis, chronic fatigue syndrome or subacute sclerosing panencephalitis) and primary lymphadenopathy-associated illnesses, and in research and development, including screening of potential new antiviral drugs. The nucleic acid, protein and the viral particle are useful in manufacturing a vaccine. The protein is also used in producing a Cryptovirus specific antibody. The antibody may also be used in manufacturing a medicament for the treatment of Cryptovirus infections. The polynucleotides of the invention can be used to treat disorders by gene therapy. This

CC Polynucleotide sequence represents the coding DNA for the human Cryptovirus strain BBR protein of the invention

CC Sequence 15246 BP; 4753 A; 3273 C; 3131 G; 4089 T; 0 U; 0 Other;

SQ

Query Match 82.0%; Score 16.4; DB 7; Length 15246;

Best Local Similarity 94.4%; Pred. No. 3.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATACTCATGTTGATG 20

Db 13125 TCCATACTCATGTTGATG 13108

RESULT 15

ABA90521\_15

Continuation (16 of 24) of ABA90521 from base 1500001 (Genomic sequence of Lactococcus l

WP Sequence split into 24 fragments LOCUS ABA90521 Accession Aba90521

Fragment Name	Begin	End
ABA90521_00	1	110000
ABA90521_01	100001	210000
ABA90521_02	200001	310000
ABA90521_03	300001	410000
ABA90521_04	400001	510000
ABA90521_05	500001	610000
ABA90521_06	600001	710000
ABA90521_07	700001	810000
ABA90521_08	800001	910000
ABA90521_09	900001	1010000
ABA90521_10	1000001	1110000
ABA90521_11	1100001	1210000
ABA90521_12	1200001	1310000
ABA90521_13	1300001	1410000
ABA90521_14	1400001	1510000
ABA90521_15	1500001	1610000
ABA90521_16	1600001	1710000
ABA90521_17	1700001	1810000
ABA90521_18	1800001	1910000
ABA90521_19	1900001	2010000
ABA90521_20	2000001	2110000
ABA90521_21	2100001	2210000
ABA90521_22	2200001	2310000
ABA90521_23	2300001	2365589

WP

Query Match 82.0%; Score 16.4; DB 6; Length 11000;

Best Local Similarity 94.4%; Pred. No. 4.8e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATACTCATGTTGATG 20

Db 51686 TCCATACTCATGTTGATG 51703

RESULT 16

ABA97710/c

ID ABA97710 standard; cDNA; 431 BP.

XX

AC ABA97710;

XX

DT 14-JAN-2003 (first entry)

XX Human pancreatic cancer expressed cDNA SEQ ID NO 3118.

DE

XX Human: pancreas; cancer; gene therapy; vaccine; immunostimulant;

KW

XX Human: pancreas; cancer; gene therapy; vaccine; immunostimulant; cytotoxic; tumour; gene; ss.

XX Homo sapiens.

OS

XX WO200260317-A2.

DN

XX 08-AUG-2002.

PP 30-JAN-2002; 2002WO-US002781.

XX	PR	30-JAN-2001; 2001US-0265305P.
XX	PR	31-JAN-2001; 2001US-0265682P.
XX	PR	09-FEB-2001; 2001US-0267568P.
XX	PR	21-MAR-2001; 2001US-0278651P.
XX	PR	28-APR-2001; 2001US-0287112P.
XX	PR	16-MAY-2001; 2001US-0291631P.
XX	PR	12-JUL-2001; 2001US-0315484P.
XX	PR	20-AUG-2001; 2001US-0313999P.
XX	PR	27-NOV-2001; 2001US-0333626P.
PA	PA	(CORI-) CORIXA CORP.
XX	PI	Benson DR, Kalos MD, Iodes MJ, Persing DH, Hepler WT, Jiang Y;
XX	DR	WPI; 2002-627435/67.
PT	PT	New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic cancer.
XX	PS	Claim 1; SEQ ID NO 3118; 300pp + Sequence Listing; English.
CC	CC	The invention relates to an isolated polynucleotide (1) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a) under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68395-ABP8637) encoded by (1) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridization, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <a href="http://ftp.wipo.int/pub/published_pct Sequences">ftp.wipo.int/pub/published_pct Sequences</a>
CC	CC	Sequence 431 BP; 150 A; 63 C; 60 G; 156 T; 0 U; 2 Other;
CC	CC	Query Match 79.0%; Score 15.8; DB 6; Length 431; Best Local Similarity 89.5%; Pred. No. 4.6e-02; Mismatches 17; Conservative 0; Mismatches+2; Indels 0; Gaps 0;
SQ	Qy	2 GTCCCTACTCATGTGATG 20
Db	Db	194 GTCCATAATCAAGTGTGATG 176
RESULT 17	RESULT 18	AAA16057
AC	ID	AAA16057 Standard; DNA; 614 BP.
AC	XX	
AC	AC	AAA16057;
AC	XX	
AC	DT	14-JUN-2000 (first entry)
XX	DB	Human colon cancer differentially expressed nucleotide sequence #62.
XX	XX	
XX	KW	Colon cancer; detect; differential expression; human; treatment; detect mutation; non-invasive diagnostic method; ds.
DB	KW	
OS	OS	Homo sapiens.
XX	XX	
XX	PN	US2003073623-11.
XX	PR	17-APR-2003.
XX	PR	30-JUL-2001; 2001US-00918995.
PA	PA	(DRMA/ ) DRMANAC R T.
PA	PA	(LAB/ ) LABAT I.
PA	PA	(STAC/ ) STACHE-CRAIN B.
PA	PA	(DICK/ ) DICKSON M C.
PA	PA	(JONE/ ) JONES L W.
XX	XX	Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX	DR	WPI; 2003-615964/58.
XX	PT	New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as Oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
XX	PS	Claim 1; SEQ ID NO 12216; 44pp; English.
CC	CC	The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH20831, whose sequence was determined by the technique of SBH (sequencing by hybridization). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleotide sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probe, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docID=2003073623
XX	SQ	Sequence 462 BP; 104 A; 120 C; 124 G; 112 T; 0 U; 2 Other;
XX	Query Match 79.0%; Score 15.8; DB 8; Length 462; Best Local Similarity 89.5%; Pred. No. 4.7e-02; Mismatches 17; Conservative 0; Mismatches+2; Indels 0; Gaps 0;	
Db	Qy	2 GTCCCTACTCATGTGATG 20
Db	Db	446 GTCCCTCTCATGTGATG 428



Query Match 79.0%; Score 15.8; DB 4; Length 6454;  
 Best Local Similarity 89.5%; Pred. No. 6.7e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy |||||||GTCCATACATCGTGTGATG 20  
 Db 1006 GTTCATACATCGTGTG 988

RESULT 21  
 ABL03787/c  
 ABL03787 standard; cDNA; 8114 BP.  
 XX  
 AC  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 5840.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 DD 27-SEP-2001.  
 XX  
 PR 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 BR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656660/75.  
 DR P-PSDB; ABB59683.  
 XX  
 PR New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions.  
 XX  
 DS Claim 1; SEQ ID NO 5840; 21pp + Sequence Listing; English.  
 XX  
 PS The invention relates to an isolated nucleic acid detection reagent  
 XX capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA  
 CC sequences (ABL0184-ABL16175) and the encoded proteins (ABB5773-  
 CC ABB2072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at [ftp.wipo.int/pub/published/pct/sequences](http://ftp.wipo.int/pub/published/pct/sequences)  
 XX  
 SQ Sequence 18737 BP; 4552 A; 4551 C; 4677 G; 4957 T; 0 U; 0 Other;

Query Match 79.0%; Score 15.8; DB 4; Length 18737;  
 Best Local Similarity 89.5%; Pred. No. 7.7e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCATACATCGTGTGAT 19  
 Db 1360 GGTCATACATCGTGTGAT 1378

RESULT 23  
 ABL03396/c  
 ID ABL03396 Standard; cDNA; 24401 BP.  
 XX  
 AC ABL03396;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4670.  
 XX  
 KW Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical; gene; ss.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN WO200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX

RESULT 22  
 ABL03786  
 ID ABL03786 standard; cDNA; 18737 BP.  
 XX  
 AC ABL03786;

PP 23-MAR-2001; 2001WO-US009231.  
 XX PR  
 PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 PR  
 PA (PEKE ) PE CORP NY.  
 XX PI Venter JC., Adams M. Li PWD, Myers EW;  
 PT WPI; 2001-656860/75.  
 DR P-PSDB; ABB59293.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signaling and cell-cell interactions.  
 PT  
 PS Claim 1; SEQ ID NO 4670; 21pp + Sequence Listing; English.  
 XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABU01840-ABL16175) and the encoded proteins (AB55773-ABY2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)  
 XX Sequence 24401 BP; 7446 A; 4747 C; 4751 G; 7457 T; 0 U; 0 Other;  
 Query Match 79.0%; Score 15.8; DB 4; Length 24401;  
 Best Local Similarity 89.5%; Pred. No. 8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 2 GTCCGATCTCTGTGTTAG 20  
 Db 12878 GTCAATACTCATGTATGATG 12860

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RESULT 24  
 ABK42099  
 ID ABK42099 standard; cDNA; 551 BP.  
 XX AC  
 XX ABK42099;  
 DT 21-MAY-2002 (first entry)  
 XX CDNA encoding novel human connective tissue related polypeptide #487.  
 XX Human; Connective tissue related disorder; cancer; gene therapy;  
 KW cytostatic; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO200155343-A1.  
 XX PD 02-AUG-2001.  
 XX PR 17-JUN-2001; 2001WO-US001322.  
 XX PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
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 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-021680P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 14-JUL-2000; 2000US-0218280P.  
 PR 26-JUL-2000; 2000US-0220963P.  
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 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
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 PR 14-AUG-2000; 2000US-0225758P.  
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 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226661P.  
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 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-028924P.  
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 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-022959P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0231968P.  
 PR 12-SEP-2000; 2000US-023197P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0232303P.  
 PR 14-SEP-2000; 2000US-02323064P.  
 PR 14-SEP-2000; 2000US-02323065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 25-SEP-2000; 2000US-0234998P.  
 PR 26-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235934P.  
 PR 27-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
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 PR 02-OCT-2000; 2000US-0236802P.  
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 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
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 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.

CC data for this patent did not form part of the printed specification, but  
 was obtained in electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 551 BP; 143 A; 94 C; 114 G; 194 T; 0 U; 6 Other;

SQ Query Match 77.0%; Score 15.4; DB 4; Length 551;  
 Best Local Similarity 94.1%; Pred No. 7.6e+02; 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TCCATFACTCATGTGAT 19  
 Db 261 TCCATTCATCTAGTGTAT 277

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RESULT 25  
 ADB5976 ID ADB5976 standard; cDNA; 551 BP.  
 XX AC ADB5976;  
 XX DT 04-DBC-2003 (first entry)

DE Connective tissue related polynucleotide #487.  
 XX cytotoxic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;  
 XX antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;  
 XX antiinflammatory; antiallergic; antiarthritic; dermatologic;  
 XX nephrotic; virucide; fungicide; antibacterial; dermatoparacitic;  
 XX gene therapy; ds; connective tissues disorder; rheumatoid arthritis;  
 XX systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;  
 XX cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;  
 XX Alzheimer's disease; Parkinson's disease; cardiovascular disease;  
 XX atherosclerosis; myocarditis; cardiopulmonary bypass complication;  
 XX autoimmune disease; multiple sclerosis; allergic reaction; asthma;  
 XX rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;  
 XX gastrointestinal disorder; inflammatory bowel disease; Bruton's disease;  
 XX organ transplant rejection; immune system disorder; Bruton's disease;  
 XX X-linked lymphoproliferative syndrome; B-cell lymphoproliferative disorder; HIV; AIDS; infection;  
 XX chromosome mapping; connective tissue related polynucleotide; gene; ss.  
 XX Homo sapiens.  
 XX US2003054375-A1.  
 XX PN 20-MAR-2003.  
 XX PD 07-MAR-2002; 2002US-00092154.  
 XX PR 31-JAN-2000; 2000US-0179065P.  
 XX PR 04-FEB-2000; 2000US-0180628P.  
 XX PR 24-FEB-2000; 2000US-0184664P.  
 XX PR 02-MAR-2000; 2000US-0184350P.  
 XX PR 16-MAR-2000; 2000US-0189874P.  
 XX PR 17-MAR-2000; 2000US-019076P.  
 XX PR 18-APR-2000; 2000US-0198123P.  
 XX PR 19-MAY-2000; 2000US-0205515P.  
 XX PR 07-JUN-2000; 2000US-0203467P.  
 XX PR 28-JUN-2000; 2000US-0214886P.  
 XX PR 30-JUN-2000; 2000US-0215135P.  
 XX PR 07-JUL-2000; 2000US-0216647P.  
 XX PR 07-JUL-2000; 2000US-0216888P.  
 XX PR 11-JUL-2000; 2000US-0217487P.  
 XX PR 14-JUL-2000; 2000US-0218290P.  
 XX PR 26-JUN-2000; 2000US-0220963P.  
 XX PR 14-AUG-2000; 2000US-0224518P.  
 XX PR 14-AUG-2000; 2000US-0224519P.  
 XX PR 14-AUG-2000; 2000US-022213P.  
 XX PR 14-AUG-2000; 2000US-0225214P.

PR 20-OCT-2000; 2000US-0241809P.  
 PR 02-OCT-2000; 2000US-0241826P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
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 PR 08-NOV-2000; 2000US-0246525P.  
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 PR 08-NOV-2000; 2000US-0246533P.  
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 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249445P.  
 PR 17-NOV-2000; 2000US-0249564P.  
 PR 17-NOV-2000; 2000US-0249565P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 01-DEC-2000; 2000US-0251869P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251989P.  
 PR 05-DEC-2000; 2000US-0251979P.  
 PR 08-DEC-2000; 2000US-0251859P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251900P.  
 PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Barash SC, Ruben SM,  
 XX WPI; 2001-565190/63.  
 DR P-PSDB; AUU86921.

PT Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis.

XX Claim 4; SEQ ID NO 497; 673pp; English.

CC The present invention relates to the isolation of novel human connective tissue related polypeptides (AUU8435-AUU86923) and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ADB41613-ABK42101 represent cDNA sequences encoding the novel human connective tissue related polypeptides. Note: The sequence

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 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
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 PR 29-SEP-2000; 2000US-0236368P.  
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 PR 29-SEP-2000; 2000US-0236370P.  
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 PR 17-NOV-2000; 2000US-0249318P.  
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 PR 17-NOV-2000; 2000US-0249315P.  
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 PR 05-JAN-2001; 2001US-00764847.  
 PR 17-JAN-2001; 2001US-00764847.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX PA  
 XX PI Rosen CA, Ruben SM, Barash SC;  
 XX DR WPI: 2003-634869/60.  
 XX P-PSDB; ADB60255.  
 XX  
 PT New connective tissue-related polypeptides and polynucleotides, useful  
 PT for treating, preventing and/or prognosis e.g. disorders of connective  
 PT tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or  
 PT neoplasias.  
 XX  
 PT Claim 1; SEQ ID NO 497; 248pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid molecule (I), which  
 CC comprises a sequence that is at least 95 % identical to a connective  
 CC tissue-related polynucleotide encoding connective tissue antigens (CTA).  
 CC The polypeptide or polynucleotide is useful for preventing, treating, or  
 CC ameliorating medical conditions in a mammal. The connective tissue  
 CC polypeptides, polynucleotides and antibodies are particularly useful for  
 CC treating, preventing and/or prognosis disorders of connective tissues  
 CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus,  
 CC scleroderma, or Sjögren's syndrome), cancers, cancer metastases and/or  
 CC neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g.  
 CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases  
 CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass  
 CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,  
 CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

Query Match

77.0%; Score 15.4; DB 8; Length 551;



XX  
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:2683.  
XX  
KW staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;  
KW endocarditis; ds.  
XX  
OS staphylococcus epidermidis.  
XX  
PN WO200134809-A2.  
XX  
PD 17-MAY-2001.  
XX  
PP 09-NOV-2000; 2000WO-US030782.  
XX  
PR 09-NOV-1999; 99US-0164258P.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PT Kimmerly WT;  
XX  
DR WPI; 2001-316495/33.  
XX  
DR P-PSDB; AG82795.

PT Nucleic acids encoding polypeptides from *Staphylococcus epidermidis*, useful for vaccinating against infections, e.g. endocarditis.  
XX  
PS Claim 8; Page 702; 2188pp; English.

XX  
AH52304 to AH53970 represent nucleic acids (I) encoding polypeptides (I), given in AG81454 to AG83120; from *Staphylococcus epidermidis*. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce host cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AH53971 to AH55090 represent specifically claimed S. epidermidis genomic DNA poly nucleotide sequences from the present invention. AH55091 to AH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the poly nucleotide sequences given in the sequence listing only listing of the present specificiation, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:445 to 4464

XX  
SQ Sequence 675 BP; 260 A; 90 C; 132 G; 192 T; 0 U; 0 Other;  
XX  
Query Match 77.0%; Score 15.4; DB 4; Length 675;  
Best Local Similarity 94.1%; Pred. No. 7.8e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 GTCCATACATCTAGTGA 18  
Db 427 GTCGATCTCATGTTGA 443

RESULT 30  
AAC46198/C  
ID AAC46198 standard; DNA; 2132 BP.  
XX  
AC AAC46198;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 49255.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control; protein identification assay; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
BN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PP 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.

RESULT 29  
ABN9025  
ID ABN9025 standard; DNA; 675 BP.  
XX  
AC ABN9025;  
XX  
DT 24-JUL-2002 (first entry)

XX  
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:388.  
XX  
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection; antibiotic; gene therapy; gene; ds.  
XX

PR 01-APR-1999; 99US-0127462P.  
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 PR 15-JUL-1999; 99US-0144055P.  
 PR 16-JUL-1999; 99US-0144085P.  
 PR 16-JUL-1999; 99US-0144085P.  
 PR 19-JUL-1999; 99US-0144325P.  
 PR 23-APR-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
 PR 19-JUL-1999; 99US-0144333P.  
 PR 19-JUL-1999; 99US-0144334P.  
 PR 19-JUL-1999; 99US-0144335P.  
 PR 20-JUL-1999; 99US-0144632P.  
 PR 20-JUL-1999; 99US-0145089P.  
 PR 21-JUL-1999; 99US-0145114P.  
 PR 21-JUL-1999; 99US-0145086P.  
 PR 21-JUL-1999; 99US-0145088P.  
 PR 22-JUL-1999; 99US-0145085P.  
 PR 22-JUL-1999; 99US-0145276P.  
 PR 22-JUL-1999; 99US-0145913P.  
 PR 22-JUL-1999; 99US-0145918P.  
 PR 23-JUL-1999; 99US-0145145P.  
 PR 23-JUL-1999; 99US-0145224P.  
 PR 23-JUL-1999; 99US-0145218P.  
 PR 23-JUL-1999; 99US-0145951P.  
 PR 23-JUL-1999; 99US-0146386P.  
 PR 02-AUG-1999; 99US-0146388P.  
 PR 02-AUG-1999; 99US-0146389P.  
 PR 03-AUG-1999; 99US-0147038P.  
 PR 04-AUG-1999; 99US-0147204P.  
 PR 04-AUG-1999; 99US-0147302P.  
 PR 05-AUG-1999; 99US-0147192P.  
 PR 05-AUG-1999; 99US-0146380P.  
 PR 06-AUG-1999; 99US-0147303P.  
 PR 06-AUG-1999; 99US-0147416P.  
 PR 09-AUG-1999; 99US-017493P.  
 PR 09-AUG-1999; 99US-0147935P.  
 PR 10-AUG-1999; 99US-0148171P.  
 PR 11-AUG-1999; 99US-0148341P.  
 PR 12-AUG-1999; 99US-0148345P.  
 PR 13-AUG-1999; 99US-0148565P.  
 PR 13-AUG-1999; 99US-0148684P.  
 PR 16-AUG-1999; 99US-0149368P.  
 PR 17-AUG-1999; 99US-0149375P.  
 PR 18-AUG-1999; 99US-0149426P.  
 PR 20-AUG-1999; 99US-0149723P.  
 PR 20-AUG-1999; 99US-0149929P.  
 PR 20-AUG-1999; 99US-0149930P.  
 PR 23-AUG-1999; 99US-0149930P.  
 PR 23-AUG-1999; 99US-0149931P.  
 PR 25-AUG-1999; 99US-0150566P.  
 PR 26-AUG-1999; 99US-015084P.  
 PR 27-AUG-1999; 99US-0151065P.  
 PR 27-AUG-1999; 99US-0151066P.  
 PR 27-AUG-1999; 99US-0151080P.  
 PR 30-AUG-1999; 99US-0151303P.  
 PR 31-AUG-1999; 99US-0151438P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153758P.  
 PR 15-SEP-1999; 99US-0156018P.  
 PR 16-SEP-1999; 99US-0156039P.  
 PR 20-SEP-1999; 99US-0157179P.  
 PR 22-SEP-1999; 99US-0155139P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0156559P.  
 PR 28-SEP-1999; 99US-015658P.  
 PR 29-SEP-1999; 99US-0156596P.  
 PR 04-OCT-1999; 99US-0157179P.  
 PR 05-OCT-1999; 99US-0157753P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158332P.  
 PR 12-OCT-1999; 99US-01583369P.



PR 20-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0144814P.  
 PR 21-JUL-1999; 99US-0145086P.  
 PR 21-JUL-1999; 99US-0145088P.  
 PR 22-JUL-1999; 99US-0145055P.  
 PR 22-JUL-1999; 99US-0145087P.  
 PR 22-JUL-1999; 99US-0145089P.  
 PR 22-JUL-1999; 99US-0145192P.  
 PR 23-JUL-1999; 99US-0145145P.  
 PR 23-JUL-1999; 99US-0145218P.  
 PR 23-JUL-1999; 99US-0145224P.  
 PR 26-JUL-1999; 99US-0145276P.  
 PR 27-JUL-1999; 99US-0145913P.  
 PR 27-JUL-1999; 99US-0145918P.  
 PR 28-JUL-1999; 99US-0145919P.  
 PR 02-AUG-1999; 99US-0145251.  
 PR 02-AUG-1999; 99US-0146386P.  
 PR 02-AUG-1999; 99US-0146388P.  
 PR 03-AUG-1999; 99US-0147032P.  
 PR 04-AUG-1999; 99US-0147192P.  
 PR 05-AUG-1999; 99US-0147303P.  
 PR 06-AUG-1999; 99US-0147460P.  
 PR 09-AUG-1999; 99US-0147493P.  
 PR 09-AUG-1999; 99US-0147935P.  
 PR 10-AUG-1999; 99US-0148171P.  
 PR 11-AUG-1999; 99US-0148319P.  
 PR 12-AUG-1999; 99US-0148341P.  
 PR 13-AUG-1999; 99US-0148565P.  
 PR 16-AUG-1999; 99US-0148634P.  
 PR 17-AUG-1999; 99US-0149175P.  
 PR 23-AUG-1999; 99US-0149426P.  
 PR 20-AUG-1999; 99US-0149722P.  
 PR 20-AUG-1999; 99US-0149723P.  
 PR 20-AUG-1999; 99US-0149802P.  
 PR 23-AUG-1999; 99US-0149930P.  
 PR 25-AUG-1999; 99US-0150566P.  
 PR 26-AUG-1999; 99US-0150884P.  
 PR 27-AUG-1999; 99US-0151065P.  
 PR 27-AUG-1999; 99US-0151080P.  
 PR 30-AUG-1999; 99US-0151303P.  
 PR 31-AUG-1999; 99US-0151438P.  
 PR 01-SEP-1999; 99US-0151930P.  
 PR 07-SEP-1999; 99US-0152363P.  
 PR 10-SEP-1999; 99US-0153070P.  
 PR 13-SEP-1999; 99US-0153788P.  
 PR 15-SEP-1999; 99US-0154018P.  
 PR 16-SEP-1999; 99US-0154039P.  
 PR 20-SEP-1999; 99US-0154779P.  
 PR 22-SEP-1999; 99US-0155139P.  
 PR 23-SEP-1999; 99US-0155486P.  
 PR 24-SEP-1999; 99US-0155639P.  
 PR 28-SEP-1999; 99US-016458P.  
 PR 29-SEP-1999; 99US-0156536P.  
 PR 04-OCT-1999; 99US-0157117P.  
 PR 05-OCT-1999; 99US-0157733P.  
 PR 06-OCT-1999; 99US-0157865P.  
 PR 07-OCT-1999; 99US-0158029P.  
 PR 08-OCT-1999; 99US-0158222P.  
 PR 12-OCT-1999; 99US-0158369P.  
 PR 13-OCT-1999; 99US-0159233P.  
 PR 13-OCT-1999; 99US-0159244P.  
 PR 13-OCT-1999; 99US-0159255P.  
 PR 14-OCT-1999; 99US-0159329P.  
 PR 14-OCT-1999; 99US-0159330P.  
 PR 14-OCT-1999; 99US-0159331P.  
 PR 14-OCT-1999; 99US-0159637P.

PR 14-OCT-1999; 99US-0159638P.  
 PR 18-OCT-1999; 99US-0159584P.  
 PR 21-OCT-1999; 99US-0160741P.  
 PR 21-OCT-1999; 99US-0160767P.  
 PR 21-OCT-1999; 99US-0160768P.  
 PR 22-OCT-1999; 99US-0160770P.  
 PR 21-OCT-1999; 99US-0160814P.  
 PR 21-OCT-1999; 99US-0160815P.  
 PR 22-OCT-1999; 99US-0160981P.  
 PR 22-OCT-1999; 99US-0160989P.  
 PR 25-OCT-1999; 99US-0161404P.  
 PR 25-OCT-1999; 99US-0161405P.  
 PR 25-OCT-1999; 99US-0161406P.  
 PR 26-OCT-1999; 99US-0161359P.  
 PR 26-OCT-1999; 99US-0161360P.  
 PR 26-OCT-1999; 99US-0161361P.  
 PR 28-OCT-1999; 99US-0161920P.  
 PR 28-OCT-1999; 99US-0161922P.  
 PR 28-OCT-1999; 99US-0161993P.  
 PR 29-OCT-1999; 99US-0162142P.

Query Match  
 Best Local Similarity 97.0%; Score 15.4; DB 3; Length 2135;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	3 TCCATACATCATGTTGAT 19
Db	39 TCCATRACTCATGGTAT 23

RESULT 32

ID	AAH54374 standard; DNA; 2946 BP.
XX	AAH54374;
AC	AAH54374;
XX	
DT	03-SEP-2001 (first entry)
DE	S. epidermidis genomic polynucleotide sequence SEQ ID NO:3738.
XX	
KW	Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination; endocarditis; ds.
XX	
OS	Staphylococcus epidermidis.
XX	
PN	W0200134809-A2.
XX	
DD	17-MAY-2001.
XX	
PP	09-NOV-2000; 2000WO-US030782.
XX	
PR	09-NOV-1999; 99US-0164258P.
XX	
PA	(GLAX ) GLAXO GROUP LTD.
XX	
PT	Kimmerly WJ;
XX	
MPI	2001-316495/33.
XX	
PT	Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.
XX	
Claim 8; Page 1360-1361; 218pp; English.	
XX	
CC	AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce host cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria.

CC The polypeptides may also be used to assay for other inhibitors of their  
 CC activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH5391 to  
 CC AAH55090 represent specifically claimed S. epidermidis genomic DNA  
 CC polynucleotide sequences from the present invention. AAH5501 to AAH55098  
 CC represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention  
 CC specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence  
 CC listing only goes up to SEQ ID NO:4454 so even though sequences are given  
 CC in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present  
 CC for SEQ ID NO:4455 to 4464

XX	Sequence 3021 BP; 948 A; 504 C; 458 G; 1111 T; 0 U; 0 Other;
CC	Query Match 77.0%; Score 15.4; DB 4; Length 3021;
CC	Best Local Similarity 94.1%; Pred. No. 9.5e+02;
CC	Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGCCATCTCATGTTGA 18  
 Db 1300 GTGAGTACTCATGTTGA 1316

RESULT 33

AAH54280/C DE AAH54393 standard; DNA; 3021 BP.

XX ID AAH54380 standard; DNA; 3021 BP.

XX AC AAH54380;

XX DT 03-SEP-2001 (first entry)

XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3744.

XX OS Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.

XX KW Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.

XX PN WO200134809-A2.

XX PD 17-MAY-2001.

XX PP 09-NOV-2000; 2000WO-US030782.

XX PR 09-NOV-1999; 99US-0164258P.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Kimmery WJ;

XX WPI; 2001-316495/33.

XX PS Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.

XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.

XX PS Claim 8; Page 1382-1383; 2188pp; English.

XX CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce host cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH5391 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH5501 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464

CC Sequence 3391 BP; 1291 A; 512 C; 581 G; 1007 T; 0 U; 0 Other;

SQ Sequence 3391 BP; 1291 A; 512 C; 581 G; 1007 T; 0 U; 0 Other;

CC specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464

XX	Sequence 3021 BP; 948 A; 504 C; 458 G; 1111 T; 0 U; 0 Other;
CC	Query Match 77.0%; Score 15.4; DB 4; Length 3021;
CC	Best Local Similarity 94.1%; Pred. No. 9.5e+02;
CC	Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGCCATCTCATGTTGA 18  
 Db 1170 GTGAGTACTCATGTTGA 1154

RESULT 34

AAH54393 DE AAH54393 standard; DNA; 3391 BP.

XX ID AAH54393;

XX AC AAH54393;

XX DT 03-SEP-2001 (first entry)

XX DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3757.

XX OS Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.

XX KW Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.

XX PN WO200134809-A2.

XX PD 17-MAY-2001.

XX PP 09-NOV-2000; 2000WO-US030782.

XX PR 09-NOV-1999; 99US-0164258P.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Kimmery WJ;

XX WPI; 2001-316495/33.

XX PS Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.

XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis.

XX PS Claim 8; Page 1382-1383; 2188pp; English.

XX CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce host cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH5391 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH5501 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464

CC Sequence 3391 BP; 1291 A; 512 C; 581 G; 1007 T; 0 U; 0 Other;



CC obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published.pct\_sequences.  
 XX Sequence 28564 BP; 7531 A; 5791 C; 5944 G; 9298 T; 0 U; 0 Other;  
 SQ Best Local Similarity 94.1%; Pred. No. 1.3e+03; Length 28564;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 GTCCATACTCGTGTGA 18  
 Db 19285 GTCCAACTCTGTGCA 19269

RESULT 37

ADD48581/C  
 ID ADD48581 standard; DNA; 28564 BP.  
 AC ADD48581;  
 XX DT 29-JAN-2004 (first entry)  
 DE Human gene AF297093; SEQ ID NO 14287.  
 XX KW Human; dr; gene; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction; injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX OS Homo sapiens.  
 XX PN WO2003016475-A2.  
 XX PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 27-FEB-2003.  
 XX PA (GEHO ) GEN HOSPITAL CORP.  
 PA (EARB ) BAYER AG.  
 XX PR 14-AUG-2002; 2002WO-US025765.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX PT New composition comprising two or more isolated polypeptides, useful for  
 preparing a medicament for treating pain in an animal.  
 XX PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human DNA (shown in Table 2 of the  
 CC specification) which encodes one of the polypeptides of the invention  
 CC which is differentially expressed during pain. Note: The sequence data  
 CC for this patient did not form part of the printed specification, but was  
 CC obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published.pct\_sequences.  
 XX Sequence 28564 BP; 7531 A; 5791 C; 5944 G; 9298 T; 0 U; 0 Other;  
 SQ Best Local Similarity 94.1%; Pred. No. 1.3e+03; Length 28564;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 GTCCATACTCGTGTGA 18  
 Db 19285 GTCCAACTCTGTGCA 19269

RESULT 38

AAI61371/C  
 ID AAI61371 standard; DNA; 339913 BP.  
 AC AAI61371;  
 XX DT 16-OCT-2001 (first entry)  
 DE Soybean 240017 region G3, SEQ ID NO: 2.  
 XX PN Soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN;  
 KW SCN resistance; rhl1; Rhg4; SCN resistant allele; plant breeding;  
 KW 240017 region G3; 318013 region A3; 515002 region G2; ds.  
 XX OS Glycine max.  
 XX PN WO200151627-A2.  
 XX PR 07-JAN-2000; 2000US-0174880P.  
 XX PA (MONS ) MONSANTO CO.  
 XX PI Hauge BM, Wang ML, Parsons JD, Parnell LD;  
 DR WPI; 2001-425872/45.  
 DR P-PSDB; AAM42214.  
 XX PT New purified nucleic acid for producing a soybean plant having soybean  
 cyst nematode resistance and for use in plant breeding programs.  
 XX PS Claim 2; Page 204-400; 1353pp; English.

The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rhl1 or an Rhg4 SCN resistant allele. The nucleic acids can be used for investigating rhl1 or Rhg4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecule provided in the specification

CC Sequence 335913 BP; 114579 A; 53403 C; 53026 G; 114905 T; 0 U; 0 Other;  
 XX Query Match 77.0%; Score 15.4; DB 5; Length 335913;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCCATACATGTTGAT 19  
 DE Human secreted protein 5' EST, SEQ ID NO: 3593.  
 XX  
 Db 24565 ||||| ||||| ||||| 24549  
 XX  
 ID AAI61372/C Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 XX gene therapy; chromosome mapping; ss.  
 XX  
 AC AAI61372; OS Homo sapiens.  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Soybean 240017 region G3, SEQ ID NO: 3.  
 XX  
 KW soybean; antihelmintic; gene therapy; soybean cyst nematode; SCN; SCN resistance; rhgl; Rbh4; SCN resistant allele; plant breeding;  
 XX  
 KW 240017 region G3; 318013 region A3; 515002 region G2; db.  
 XX  
 OS Glycine max.  
 XX  
 WO200151627-A2.  
 PN  
 XX  
 PD 19-JUL-2001.  
 XX  
 PP 05-JAN-2001; 2001WO-US000552.  
 XX  
 PR 07-JAN-2000; 2000US-0174880P.  
 XX  
 PA (MONS ) MONSANTO CO.  
 XX  
 PT Hauge BM, Wang ML, Parsons JD, Parnell LD;  
 XX  
 DR WPI; 2001-425972/45.  
 DR-P5DB; AAM42215.  
 XX  
 PT New purified nucleic acid for producing a soybean plant having soybean cyst nematode resistance and for use in plant breeding programs.  
 XX  
 PS Claim 2; Page 400-555; 1353pp; English.  
 XX  
 CC The invention relates to nucleic acid molecules from regions of the soybean genome which are associated with soybean cyst nematode (SCN) resistance. The nucleic acids are used to transform plants, and can produce soybean plants having an rgh1 or an Rbh4 SCN resistant allele.  
 CC The nucleic acids can be used for investigating rgh1 or Rbh4 haplotypes of soybean plants and for introgressing SCN resistance or partial SCN resistance into soybean plants. They can also be used in plant breeding programmes. The invention also relates to proteins encoded by such nucleic acid molecules, as well as antibodies capable of recognising these proteins. The present sequence is a nucleic acid molecule provided in the specification.  
 CC  
 SQ Sequence 335913 BP; 114582 A; 53398 C; 53027 G; 114906 T; 0 U; 0 Other;  
 Query Match 77.0%; Score 15.4; DB 5; Length 335913;  
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 TCCATACATGTTGAT 19  
 DE 24565 TCCAACTCAAGTTGAT 24549  
 XX  
 RESULT 40  
 ID AAC31848/C Computer readable medium; vaccine; S. aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
 XX skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; db.  
 AC AAC31848; OS Staphylococcus aureus.  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein 5' EST, SEQ ID NO: 3593.  
 XX  
 ID AAV75448 Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 XX gene therapy; chromosome mapping; ss.  
 XX  
 AC AAV75448; OS Homo sapiens.  
 XX  
 DT 21-FEB-2000; 2000EP-00200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487P.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PT Dumas Milne Edwards J, Ducleart A, Giordano J;  
 XX  
 DR WPI; 2000-500381/45.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.  
 XX  
 PS Claim 1; SEQ ID NO 35923; 71PP + Sequence Listing; English.  
 XX  
 CC The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors  
 XX  
 SQ Sequence 308 BP; 105 A; 54 C; 53 G; 93 T; 0 U; 3 Other;  
 Query Match 76.0%; Score 15.2; DB 3; Length 308;  
 Best Local Similarity 85.0%; Pred. No. 8.8e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGTCCATACATGTTGAT 20  
 DE 98 GATCCACCATGATGATG 79  
 DB  
 XX  
 RESULT 41  
 ID AAV75448  
 XX  
 AC AAV75448;  
 XX  
 DT 16-MAR-1999 (first entry)  
 XX  
 DE Staphylococcus aureus contig SEQ ID #1137.  
 XX  
 KW Computer readable medium; vaccine; S. aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;  
 KW skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; db.  
 XX  
 OS Staphylococcus aureus.  
 XX  
 PN EP785519-A2.  
 XX  
 PD 30-JUL-1997.

XX  
 PP 07-JAN-1997; 97EP-00100117.  
 XX  
 PR 05-JAN-1996; 96US-0009861P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Kunsch CA, Choi GH, Barash SC, Dillon RJ, Fannon MR, Rosen CA;  
 XX  
 DR WPI; 1997-374922/35.  
 XX  
 PT Poly nucleotide(s) and proteins derived from *Staphylococcus aureus* -  
 PT stored on computer readable medium and used in the production of anti-  
 PT *S.aureus* vaccines.  
 XX  
 PS Claim 1; Page 1850; 3271pp; English.  
 XX  
 CC This sequence represents one of 5191 *Staphylococcus aureus* DNA sequences  
 CC of the invention. The DNA sequences are recorded on a computer readable  
 CC medium, preferably selected from a floppy or hard disk, random access  
 memory (RAM), read-only memory (ROM) or CD ROM. Homology searches using  
 CC the *S.aureus* DNA sequences allows putative functions to be assigned so  
 CC that protein-encoding or regulatory regions of commercial, therapeutic or  
 CC industrial importance can be obtained. Specifically, sequences which are  
 CC likely to encode antigens have been identified and these polypeptides can  
 CC be used in a vaccine composition against *S.aureus* infection. The  
 CC polypeptides can also be used in a kit for the immunodetection of  
 CC *S.aureus* in a sample. *S.aureus* is implicated in numerous human diseases,  
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,  
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock  
 CC syndrome, etc. Organisms transformed with the DNA sequences  
 CC (and their fragments) are useful as primers or probes for isolating  
 CC homologues of any of the *S.aureus* DNA sequences contained on the computer  
 CC readable medium.  
 SQ Sequence 330 BP; 108 A; 48 C; 54 G; 116 T; 0 U; 4 Other;  
 Query Match 76.0%; Score 15.2; DB 2; Length 330;  
 Best Local Similarity 85.0%; Pred. No. 8.9e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGTCCATACTCGTGTGATG 20  
 Db 284 GGACCAAACTCATGGATG 303  
 RESULT 42  
 AAD50058  
 ID AAD50058 standard; DNA; 443 BP.  
 XX  
 AC AAD50058;  
 XX  
 DT 24-MAR-2003 (first entry)  
 XX  
 DE Human fatty acid elongation enzyme-like protein DNA #15.  
 XX  
 KW Human; cancer; diabetes; CNS disorder; metabolic disease; asthma; COPD;  
 KW long chain polyunsaturated fatty acid elongation enzyme-like protein;  
 KW nootropic; neuroprotective; antiinflammatory; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200264761-A2.  
 PD 22-AUG-2002.  
 XX  
 PR 07-FEB-2002; 2002WO-EP001260.  
 XX  
 PS 09-FEB-2001; 2001US-0267415P.  
 PR 16-NOV-2001; 2001US-0331459P.  
 PR 04-DEC-2001; 2001US-0334928P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Zhu Z;  
 XX  
 DR WPI; 2003-040508/03.  
 XX  
 PT Human long chain fatty acid elongation enzyme-like protein is regulated  
 PT in the treatment of diseases e.g. cancer, diabetes and CNS disorders.  
 XX  
 PS Disclosure; Fig 17; 175pp; English.  
 XX  
 CC The invention relates to an isolated poly nucleotide encoding a long chain  
 CC polyunsaturated fatty acid elongation enzyme-like protein polypeptide.  
 CC The invention is useful in the preparation of a medicament for modulating  
 CC the activity/function of long chain polyunsaturated fatty acid elongation  
 CC enzyme-like protein in a disease specifically cancer, diabetes, a CNS  
 CC disorder, metabolic disease, asthma or COPD. The present sequence is  
 CC human long chain polyunsaturated fatty acid elongation enzyme-like  
 CC protein DNA.  
 XX  
 Sequence 443 BP; 170 A; 68 C; 66 G; 139 T; 0 U; 0 Other;  
 SQ Query Match 76.0%; Score 15.2; DB 7; Length 443;  
 Best Local Similarity 85.0%; Pred. No. 9.3e-02; 3; Mismatches  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GGTCCATACTCGTGTGATG 20  
 Db 422 GATCCACAAATCGTGTGATG 441  
 RESULT 43  
 AAF11349/c  
 ID AAF11349 standard; cDNA; 468 BP.  
 XX  
 AC AAF11349;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Aspergillus niger EST SEQ ID NO:3872.  
 XX  
 KW Multiple gene expression; filamentous fungal cell; EST;  
 KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;  
 KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;  
 KW culture condition; environmental stress; spore morphogenesis;  
 KW metabolic pathway; engineering; catabolic pathway engineering; ss.  
 XX  
 OS Aspergillus niger.  
 XX  
 PN WO200056762-A2.  
 XX  
 PD 28-SEP-2000.  
 XX  
 PR 22-MAR-2000; 2000WO-US007781.  
 XX  
 PR 22-MAR-1999; 99US-00273623.  
 XX  
 PA (NOVO ) NOVO NORDISK BIOTECH INC.  
 PA (NOVO ) NOVO NORDISK AS.  
 XX  
 PI Berka RM, Rey NW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
 XX  
 DR WPI; 2000-594572/56.  
 XX  
 PT Monitoring differential expression of genes in filamentous fungal cells  
 PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
 PT substrate of expressed sequence tags.  
 XX  
 PS Claim 87; Page 1730; 3161pp; English.  
 XX  
 CC The present invention describes a method for monitoring differential  
 CC expression of genes in a first filamentous fungal (FF) cell relative to  
 CC expression of the same genes in one or more second filamentous fungal

CC cells. The method uses fluorescence-labeled nucleic acids isolated from CC the FP cells and a substrate of expressed sequence tags (EST). The ESTs CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the CC global expression of genes from FP cells allows the production potential CC of the microorganisms to be improved. New genes may be discovered, CC possible functions of unknown open reading frames can be identified and CC gene copy number variation and stability can be monitored. The expression CC of genes can be used to study how FF cells adapt to changes in culture CC conditions, environmental stresses, spore morphogenesis, recombination, CC metabolic or catabolic pathway engineering. Using ESTs provides several CC advantages over genomic or random cDNA clones including elimination of CC redundancy as one spot on an array equals one gene or open reading frame, CC and organisation of the microarrays based on function of the gene CC products to facilitate analysis of the results. AF07478 to AF11247 represents ESTs from Aspergillus niger; AF11248 to AF11854 represents ESTs from Aspergillus oryzae; and AF114879 to AAFF5337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.

SQ Sequence 468 BP; 109 A; 129 C; 118 G; 111 T; 0 U; 1 Other;

Query Match 76.0%; Score 15.2; DB 3; Length 468;

Best Local Similarity 85.0%; Pred. No. 9.4e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCATACATCTGTTGATG 20

Db 102 GGTCATACATCTGTTGATG 83

RESULT 44

ID AAD50056 standard; DNA; 472 BP.

XX AAD50056;

XX AC

DT 24-MAR-2003 (first entry)

DE Human fatty acid elongation enzyme-like protein DNA #13.

XX Human; cancer; diabetes; CNS disorder; metabolic disease; asthma; COPD; KW long chain polyunsaturated fatty acid elongation enzyme-like protein; KW nootropic; neuroprotective; antiinflammatory; ds.

XX OS Homo sapiens.

XX PN WO200264761-A2.

XX PD 22-AUG-2002.

XX PR 07-FEB-2002; 2002WO-EP001260.

PR 09-FEB-2001; 2001US-0267415P.

PR 16-NOV-2001; 2001US-0331449P.

PR 04-DEC-2001; 2001US-0334948P.

XX PA (FARB ) BAYER AG.

XX PT Human long chain fatty acid elongation enzyme-like protein is regulated by Zhu Z; Disclosure; Fig 15; 175pp; English.

The invention relates to an isolated polynucleotide encoding a long chain polyunsaturated fatty acid elongation enzyme-like protein polypeptide. The invention is useful in the preparation of a medicament for modulating

CC the activity/function of long chain polyunsaturated fatty acid elongation CC enzyme-like protein in a disease specifically cancer, diabetes, a CNS CC disorder, metabolic disease, asthma or COPD. The present sequence is CC human long chain polyunsaturated fatty acid elongation enzyme-like CC protein DNA

SQ Sequence 472 BP; 174 A; 72 C; 74 G; 152 T; 0 U; 0 Other;

XX ID ABK69101/C

XX ABK69101 standard; cDNA; 479 BP.

XX AC ABK69101;

XX DT 02-JUL-2002 (first entry)

XX DE DNA encoding human secreted protein, SEQ ID No 25.

XX Human; secreted protein; autoimmune disease; rheumatoid arthritis; KW hyperproliferative disorder; neoplasm; breast; liver; ischaemia; KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder; KW angiogenesis; nervous system disorder; Alzheimer's disease; infection; KW corneal infection; wound healing; ocular disorder; skin aging; sunburn; KW epithelial cell proliferation; organ transplantation; food additive; KW food storage; gene; ss.

XX OS Homo sapiens.

XX PN WO200224721-A1.

XX PD 28-MAR-2002.

XX PR 09-JAN-2001; 2001WO-US000544.

XX PR 20-SEP-2000; 2000US-0234211P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Komatoulis GA, Baker KP, Rosen CA, Birse CE, Soppet DR; PI Olsen HS, Ni J, Fiscella M, Moore PA, Wei P, Ebner R, Duan DR; PI Shi Y, Choi GH; DR WPI; 2002-330012/36.

XX DR P-PSDB; AU96100.

XX PT Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.

XX Claim 1; Page 462; 562pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) encoding a human secreted protein (II). (I) and (II) are used to prevent, treat or CC ameliorate a medical condition in e.g. humans, mice, rabbits, goats, CC horses, cats, dogs, chickens or sheep. (I) and (II) are also used in CC diagnosing a pathological condition or susceptibility to a pathological CC condition. The antibodies to (II) can also be used in alleviating CC symptoms associated with the disorders and in diagnostic immunoassays CC e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). CC Disorders which are diagnosed or treated include autoimmune diseases e.g. CC rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the CC breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous CC system disorders e.g. Alzheimer's disease, infections caused by bacteria, CC viruses and fungi and ocular disorders e.g. corneal infection. The

CC polypeptides can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues and in chemotaxis. The polypeptides can also be  
 CC used as a food additive or preservative to increase or decrease storage  
 CC capabilities. ABK69078-ABK69143 represent human secreted protein coding  
 CC sequences, PCR primers and related sequences used in cloning and  
 CC expression of the secreted proteins described in examples of the  
 CC invention

XX Sequence 479 BP; 105 A; 169 C; 107 G; 97 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 6; Length 479;  
 Best Local Similarity 85.0%; Pred. No. 9.4e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCTCCCATACTCGTGTGATG 20

Db 373 GGTCCGTCCTAGTGATG 354

RESULT 46

ID AAD5057/c

ID AAD5057 standard; DNA; 499 BP.

XX AC AAD5057;

XX DT 24-MAR-2003 (first entry)

XX DE Human fatty acid elongation enzyme-like protein DNA #14.

XX KW Human; cancer; diabetes; CNS disorder; metabolic disease; asthma; COPD;

XX KW long chain polyunsaturated fatty acid elongation enzyme-like protein;

XX KW nootropic; neuroprotective; antiinflammatory; ds.

XX OS Homo sapiens.

XX PN WO200264761-A2.

XX PD 22-AUG-2002.

XX PF 07-FEB-2002; 2002WO-EP001260.

XX PR 09-FEB-2001; 2001US-0267415P.

XX PR 16-NOV-2001; 2001US-0331449P.

XX PR 04-DEC-2001; 2001US-0334948P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Komatsoulis GA, Baker KP, Rosen CA, Birse CE, Soppet DR,  
 PI Olsen HS, Ni J, Fiscella M, Moore PA, Wei P, Ebner R, Duan DR;  
 PI Shi Y, Choi GH;

XX DR P-PSDB; AAU96210.

XX PT Isolated nucleic acid molecule encoding a human secreted protein is used  
 PT in preventing, treating or ameliorating a medical condition.

XX PS Claim 1; Page 484; 562pp; English.

XX PA The invention relates to an isolated nucleic acid molecule (I) encoding a  
 CC human secreted protein (II). (I) and (II) are used to prevent, treat or  
 CC ameliorate a medical condition in e.g. humans, mice, rabbits, goats,  
 CC horses, cats, dogs, chickens or sheep. (I) and (II) are also used in  
 CC diagnosing a pathological condition or susceptibility to a pathological  
 CC condition. The antibodies to (II) can also be used in alleviating  
 CC symptoms associated with the disorders and in diagnostic immunoassays  
 CC e.g. radiimmunoassays or enzyme linked immunosorbent assays (ELISA).  
 CC Disorders which are diagnosed or treated include autoimmune diseases e.g.  
 CC rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the  
 CC breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular  
 CC disorders e.g. cerebral ischaemia, angiogenesis, nervous system  
 CC disorders e.g. Alzheimer's disease, infections caused by bacteria,  
 CC viruses and fungi and ocular disorders e.g. corneal infection. The  
 CC polypeptides can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues and in chemotaxis. The polypeptides can also be  
 CC used as a food additive or preservative to increase or decrease storage  
 CC capabilities. ABK69078-ABK69143 represent human secreted protein coding  
 CC sequences, PCR primers and related sequences used in cloning and  
 CC expression of the secreted proteins described in examples of the  
 CC invention

XX Sequence 547 BP; 119 A; 185 C; 121 G; 117 T; 0 U; 5 Other;

Query Match 76.0%; Score 15.2; DB 7; Length 499;  
 Best Local Similarity 85.0%; Pred. No. 9.4e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTCCCATACTCGTGTGATG 20

Db 304 GATCCGAACTCATGTTGATG 285

RESULT 47

ID ABK69131/C

ID ABK69131 standard; cDNA; 547 BP.

XX AC ABK69131;

XX DT 02-JUL-2002 (first entry)

XX DE DNA encoding human secreted protein, SEQ ID No 55.

XX KW Human; secreted protein; autoimmune disease; rheumatoid arthritis;  
 KW hyperproliferative disorder; neoplasm; breast; liver; ischaemia;  
 KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
 KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;  
 KW cornual infection; wound healing; ocular disorder; skin aging; sunburn;  
 KW epithelial cell proliferation; organ transplantation; food additive;  
 KW food storage; gene; ss.

XX OS Homo sapiens.

XX PN WO200224721-A1.

XX PD 28-MAR-2002.

XX PR 09-JAN-2001; 2001WO-US000544.

XX PR 20-SBP-2000; 2000US-0234211P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Komatsoulis GA, Baker KP, Rosen CA, Birse CE, Soppet DR,  
 PI Olsen HS, Ni J, Fiscella M, Moore PA, Wei P, Ebner R, Duan DR;  
 PI Shi Y, Choi GH;

XX DR P-PSDB; AAU96210.

XX PT Isolated nucleic acid molecule encoding a human secreted protein is used  
 PT in preventing, treating or ameliorating a medical condition.

XX PS Claim 1; Page 484; 562pp; English.

XX PA The invention relates to an isolated nucleic acid molecule (I) encoding a  
 CC human secreted protein (II). (I) and (II) are used to prevent, treat or  
 CC ameliorate a medical condition in e.g. humans, mice, rabbits, goats,  
 CC horses, cats, dogs, chickens or sheep. (I) and (II) are also used in  
 CC diagnosing a pathological condition or susceptibility to a pathological  
 CC condition. The antibodies to (II) can also be used in alleviating  
 CC symptoms associated with the disorders and in diagnostic immunoassays  
 CC e.g. radiimmunoassays or enzyme linked immunosorbent assays (ELISA).  
 CC Disorders which are diagnosed or treated include autoimmune diseases e.g.  
 CC rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the  
 CC breast or liver, cardiovascular disorders e.g. cardiac arrest,  
 CC cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous  
 CC system disorders e.g. Alzheimer's disease, infections caused by bacteria,  
 CC viruses and fungi and ocular disorders e.g. corneal infection. The  
 CC polypeptides can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues and in chemotaxis. The polypeptides can also be  
 CC used as a food additive or preservative to increase or decrease storage  
 CC capabilities. ABK69078-ABK69143 represent human secreted protein coding  
 CC sequences, PCR primers and related sequences used in cloning and  
 CC expression of the secreted proteins described in examples of the  
 CC invention

XX Sequence 547 BP; 119 A; 185 C; 121 G; 117 T; 0 U; 5 Other;

Query Match 76.0%; Score 15.2; DB 6; Length 547;  
 Best Local Similarity 85.0%; Pred. No. 9.5e+02; Mismatches 3; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTTGATG 20  
 Db 366 GTCCTCTGCTCATGTCATG 347

RESULT 48

AAD50054 standard; DNA; 548 BP.

ID AAD50054;  
 XX  
 AC  
 XX  
 DT 24-MAR-2003 (first entry)

XX Human fatty acid elongation enzyme-like protein DNA #11.  
 KW Human; cancer; diabetes; CNS disorder; metabolic disease; asthma; COPD;  
 KW long chain polyunsaturated fatty acid elongation enzyme-like protein;  
 KW nootropic; neuroprotective; antiinflammatory; ds.  
 XX OS Homo sapiens.  
 DN XX  
 PR WO200264761-A2.  
 PD 22-AUG-2002.

XX XX  
 PR 07-FEB-2002; 2002WO-EP001260.  
 PR 09-FEB-2001; 2001US-0267415P.  
 PR 16-NOV-2001; 2001US-031449P.  
 PR 04-DEC-2001; 2001US-0334948P.

XX (FARB ) BAYER AG.  
 XX PT Zhu Z.;  
 DR XX  
 PN WO200264761-A2.  
 XX 22-AUG-2002.

XX 07-FEB-2002; 2002WO-EP001260.

XX 09-FEB-2001; 2001US-0267415P.  
 PR 16-NOV-2001; 2001US-031449P.  
 PR 04-DEC-2001; 2001US-0334948P.

XX (FARB ) BAYER AG.  
 XX PT Zhu Z.;  
 XX DR WPI; 2003-040508/03.

XX Human long chain fatty acid elongation enzyme-like protein is regulated  
 PT in the treatment of diseases e.g. cancer, diabetes and CNS disorders.  
 XX Disclosure; Fig 12; 175pp; English.

XX The invention relates to an isolated polynucleotide encoding a long chain  
 CC polyunsaturated fatty acid elongation enzyme-like protein polypeptide.  
 CC The invention is useful in the preparation of a medicament for modulating  
 CC the activity/function of long chain polyunsaturated fatty acid elongation  
 CC enzyme-like protein in a disease specifically cancer, diabetes, a CNS  
 CC disorder, metabolic disease, asthma or COPD. The present sequence is  
 CC human long chain polyunsaturated fatty acid elongation enzyme-like  
 CC protein DNA.

XX Sequence 578 BP; 199 A; 87 C; 87 G; 205 T; 0 U; 0 Other;  
 PT Human long chain fatty acid elongation enzyme-like protein is regulated  
 PT in the treatment of diseases e.g. cancer, diabetes and CNS disorders.  
 XX Disclosure; Fig 13; 175pp; English.

CC The invention relates to an isolated polynucleotide encoding a long chain  
 CC polyunsaturated fatty acid elongation enzyme-like protein polypeptide.  
 CC The invention is useful in the preparation of a medicament for modulating  
 CC the activity/function of long chain polyunsaturated fatty acid elongation  
 CC enzyme-like protein in a disease specifically cancer, diabetes, a CNS  
 CC disorder, metabolic disease, asthma or COPD. The present sequence is  
 CC human long chain polyunsaturated fatty acid elongation enzyme-like  
 CC protein DNA.

XX Sequence 548 BP; 192 A; 84 C; 86 G; 186 T; 0 U; 0 Other;  
 PT Human long chain fatty acid elongation enzyme-like protein is regulated  
 PT in the treatment of diseases e.g. cancer, diabetes, a CNS  
 XX Disclosure; Fig 13; 175pp; English.

CC The invention is useful in the preparation of a medicament for modulating  
 CC the activity/function of long chain polyunsaturated fatty acid elongation  
 CC enzyme-like protein in a disease specifically cancer, diabetes, a CNS  
 CC disorder, metabolic disease, asthma or COPD. The present sequence is  
 CC human long chain polyunsaturated fatty acid elongation enzyme-like  
 CC protein DNA.

SQ RESULT 49

Query Match 76.0%; Score 15.2; DB 7; Length 548;  
 Best Local Similarity 85.0%; Pred. No. 9.5e+02; Mismatches 3; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTTGATG 20  
 Db 422 GATCCACATCANGTTGATG 441

RESULT 50

AAFI14157 standard; cDNA; 685 BP.

ID AAFI14157  
 XX  
 AC AAFI14157;  
 XX  
 DT 13-MAR-2001 (first entry)

XX Aspergillus oryzae EST SEQ ID NO:6680.

DE XX Multiple gene expression; filamentous fungal cell; EST; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.

XX OS Aspergillus oryzae.  
 XX WO200056762-A2.

XX 28-SEP-2000.

PD XX  
 PR 22-MAR-2000; 2000WO-US007781.

XX

AAD50053 standard; DNA; 578 BP.

ID AAD50053;  
 XX  
 AC AAD50053;  
 XX  
 DT 24-MAR-2003 (first entry)

XX  
PR 22-MAR-1999; 99US-00273623.  
XX  
PA (NOVO ) NOVO NORDISK BIOTECH INC.  
PA (NOVO ) NOVO NORDISK AS.

XX  
PT Berka RM, Rey MM, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;  
DR WPI; 2000-594572/56.

XX  
PT Monitoring differential expression of genes in filamentous fungal cells  
PT uses fluorescence-labeled nucleic acids isolated from the cells and a  
substrate of expressed sequence tags.  
XX  
PS Claim 88; Page 2728-2729; 3161pp; English.

CC The present invention describes a method for monitoring differential  
CC expression of genes in a first filamentous fungal (FF) cell relative to  
CC expression of the same genes in one or more second filamentous fungal  
CC cells. The method uses fluorescence-labeled nucleic acids isolated from  
CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs  
CC are used in the methods for monitoring differential expression of genes  
CC in a first filamentous fungal (FF) cell relative to expression of the  
same genes in one or more second filamentous fungal cells. Monitoring the  
global expression of genes from FF cells allows the production potential  
of the microorganisms to be improved. New genes may be discovered,  
possible functions of unknown open reading frames can be identified and  
gene copy number variation and stability can be monitored. The expression  
of genes can be used to study how FF cells adapt to changes in culture  
conditions, environmental stress, spore morphogenesis, recombination,  
metabolic or catabolic pathway engineering. Using ESTs provides several  
advantages over genomic or random cDNA clones including elimination of  
redundancy as one spot on an array equals one gene or open reading frame,  
and organisation of the microarrays based on function of the gene  
products to facilitate analysis of the results. AAF07478 to AAF11247  
represents ESTs from Fusarium venenatum; AAF11248 to AAF1183 represents  
ESTs from Aspergillus niger; AAF1184 to AAF14878 represents ESTs from  
Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from  
Trichoderma reesei, which are all specifically claimed in the present  
invention  
XX  
SQ sequence 685 BP; 169 A; 178 C; 174 G; 164 T; 0 U; 0 Other;

Query Match 76.0%; Score 15.2; DB 3; Length 685;  
Best Local Similarity 85.0%; Pred. No. 9 8e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qv 1 GGTCCATACTAGTGATG 20  
Db 353 GGTCCATACTAGTGATG 372

Search completed: August 17, 2004, 14:36:28  
Job time : 402 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: August 17, 2004, 14:16:42 , Search time 2541 seconds  
(without alignments)  
235.043 Million cell updates/sec

Title:

US-09-825-489-3

Perfect score: 20

Sequence: 1 ggccatcaactatgttgatg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 800 summaries

Database : EST:\*

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1: em_estba:*
2: em_estchum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pbln:*
20: em_gss_vrt:*
21: em_gss_fln:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rdd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	20	100.0	219 12	BG201597
C 2	20	100.0	221 12	BG212172
C 3	20	100.0	352 12	BG105555
C 4	20	100.0	359 14	BG852193
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C				

Score No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	78	16.8	84.0	730	12	BH296724	c	151	15.8	79.0	404	9	A146339
	79	16.8	84.0	757	14	CB511930	c	152	15.8	79.0	411	9	A162472
	80	16.8	84.0	789	29	CNS0815	c	153	15.8	79.0	413	9	AL564616
	81	16.8	84.0	811	29	CG255961	c	154	15.8	79.0	415	14	H05220
	82	16.8	84.0	819	29	A1414080	c	155	15.8	79.0	419	10	AW273418
	83	16.8	84.0	830	28	BH710049	c	156	15.8	79.0	443	13	BQ973507
	84	16.8	84.0	853	28	BH086317	c	157	15.8	79.0	444	9	A149900
	85	16.8	84.0	870	13	BH840815	c	158	15.8	79.0	444	9	A156466
	86	16.8	84.0	984	29	CNS0815	c	159	15.8	79.0	450	10	BF894540
	87	16.8	84.0	1682	10	BP572295	c	160	15.8	79.0	451	28	A0917107
	88	16.8	84.0	295	15	BB286508	c	161	15.8	79.0	452	14	N25549
	89	16.8	82.0	363	14	CE554445	c	162	15.8	79.0	453	9	AA800564
	90	16.8	82.0	400	28	A0011724	c	163	15.8	79.0	456	10	AW159541
	91	16.8	82.0	404	28	AC085335	c	164	15.8	79.0	457	14	CD28195
	92	16.8	82.0	475	28	BH314540	c	165	15.8	79.0	461	28	BH883167
	93	16.8	82.0	513	28	BH860919	c	166	15.8	79.0	469	10	BF435867
	94	16.8	82.0	522	29	BB652083	c	167	15.8	79.0	470	14	H02898
	95	16.8	82.0	602	29	CE524885	c	168	15.8	79.0	471	9	YJ3903.81
	96	16.8	82.0	620	14	CM548188	c	169	15.8	79.0	475	12	B1582117
	97	16.8	82.0	626	28	AC0286992	c	170	15.8	79.0	477	10	AW570406
	98	16.8	82.0	668	28	AZ333406	c	171	15.8	79.0	477	28	AQ814813
	99	16.8	82.0	672	10	BP053667	c	172	15.8	79.0	479	9	AA725575
	100	16.8	82.0	702	28	A2434015	c	173	15.8	79.0	481	10	BE074235
	101	16.8	82.0	775	14	CA423356	c	174	15.8	79.0	483	28	AQ689450
	102	16.8	82.0	775	28	BH483076	c	175	15.8	79.0	485	12	BM144849
	103	16.8	82.0	779	29	BK13283	c	176	15.8	79.0	486	12	BM769521
	104	16.8	82.0	805	28	BH313463	c	177	15.8	79.0	487	12	BT865259
	105	16.8	82.0	824	28	AZ174590	c	178	15.8	79.0	497	9	A1889130
	106	16.8	82.0	831	29	CC511858	c	179	15.8	79.0	508	14	CA735557
	107	16.8	82.0	914	13	BH274272	c	180	15.8	79.0	512	9	A1959175
	108	16.8	82.0	958	28	A0743158	c	181	15.8	79.0	512	28	AZ268834
	109	16.8	82.0	1002	10	BK016227	c	182	15.8	79.0	514	14	CD085136
	110	16.8	82.0	1220	11	AK032870	c	183	15.8	79.0	516	28	BZ916626
	111	16.8	82.0	1623	11	AK030322	c	184	15.8	79.0	518	10	BE83251
	112	16.8	82.0	1800	14	HA6770	c	185	15.8	79.0	523	10	AM270635
	113	16.8	82.0	278	13	AK013301	c	186	15.8	79.0	526	28	BZ221678
	114	16.8	82.0	576	12	BJ053329	c	187	15.8	79.0	527	13	BUT13949
	115	16.8	82.0	600	10	BR936583	c	188	15.8	79.0	533	13	BU950227
	116	16.8	82.0	636	29	CG851717	c	189	15.8	79.0	537	12	BT88105
	117	16.8	82.0	663	29	AW367203	c	190	15.8	79.0	541	9	AV91909
	118	16.8	82.0	775	10	BB243298	c	191	15.8	79.0	546	13	BU927775
	119	16.8	82.0	800	14	HA091805	c	192	15.8	79.0	548	12	BI498599
	120	16.8	82.0	270	14	CA496164	c	193	15.8	79.0	552	9	A195898
	121	16.8	82.0	270	14	CB215300	c	194	15.8	79.0	554	12	BG524360
	122	16.8	82.0	273	10	AW367203	c	195	15.8	79.0	557	9	AL045488
	123	16.8	82.0	275	9	AB659503	c	196	15.8	79.0	560	28	AQ690181
	124	16.8	82.0	275	10	AN196133	c	197	15.8	79.0	564	10	AM270635
	125	16.8	79.0	278	13	BM151316	c	198	15.8	79.0	564	14	CF032818
	126	15.8	79.0	290	14	CF087871	c	199	15.8	79.0	574	10	BF382660
	127	15.8	79.0	297	14	R24247	c	200	15.8	79.0	575	9	CE756403
	128	15.8	79.0	299	28	CC015488	c	201	15.8	79.0	579	29	CEB39041
	129	15.8	79.0	313	12	BM510485	c	202	15.8	79.0	584	10	BF648403
	130	15.8	79.0	314	13	BQ582223	c	203	15.8	79.0	587	13	BX487241
	131	15.8	79.0	317	12	BM511316	c	204	15.8	79.0	589	13	AQ985886
	132	15.8	79.0	327	13	BH918258	c	205	15.8	79.0	590	28	CD421903
	133	15.8	79.0	329	14	R91378	c	206	15.8	79.0	592	14	CB163502
	134	15.8	79.0	343	12	BI608116	c	207	15.8	79.0	593	28	AZ405088
	135	15.8	79.0	347	14	N20854	c	208	15.8	79.0	599	10	AW673731
	136	15.8	79.0	358	14	D62710	c	209	15.8	79.0	599	13	AD038485
	137	15.8	79.0	362	10	AW651621	c	210	15.8	79.0	600	28	BZ231495
	138	15.8	79.0	362	29	CG943525	c	211	15.8	79.0	600	28	BZ375237
	139	15.8	79.0	374	12	AQ01510	c	212	15.8	79.0	605	28	CEB39041
	140	15.8	79.0	388	9	AI59644	c	213	15.8	79.0	611	14	CB883863
	141	15.8	79.0	388	9	AL080028	c	214	15.8	79.0	615	28	BF74016
	142	15.8	79.0	389	14	HA1924	c	215	15.8	79.0	620	14	CF307533
	143	15.8	79.0	384	12	BM782600	c	216	15.8	79.0	622	14	CF08709
	144	15.8	79.0	388	9	A149027	c	217	15.8	79.0	631	13	BQ410891
	145	15.8	79.0	390	9	AI59644	c	218	15.8	79.0	635	14	CD014962
	146	15.8	79.0	388	12	BI055583	c	219	15.8	79.0	638	28	AQ60236
	147	15.8	79.0	389	14	H41924	c	220	15.8	79.0	645	14	CB883863
	148	15.8	79.0	391	14	N20864	c	221	15.8	79.0	653	13	BY722968
	149	15.8	79.0	395	14	CF1846400	c	222	15.8	79.0	658	28	AZ282626
	150	15.8	79.0	398	12	BI074444	c	223	15.8	79.0	661	28	BZ006698

C 224	15.8	79.0	666	29	CG760052	c 297	15.4	77.0	352	12	BT77144
C 225	15.8	79.0	668	14	CD079743	c 298	15.4	77.0	365	28	AZ255310
C 226	15.8	79.0	673	14	CB449974	c 299	15.4	77.0	372	9	AA36945
C 227	15.8	79.0	673	14	CB449974	c 300	15.4	77.0	376	9	AI85179
C 228	15.8	79.0	675	29	CG855018	c 301	15.4	77.0	380	14	CF50831
C 229	15.8	79.0	676	12	BW468848	c 302	15.4	77.0	381	9	A1216097
C 230	15.8	79.0	679	29	CG661268	c 303	15.4	77.0	386	12	BG232692
C 231	15.8	79.0	695	28	BH506396	c 304	15.4	77.0	392	13	BY605976
C 232	15.8	79.0	699	9	AV938999	c 305	15.4	77.0	393	9	AA776819
C 233	15.8	79.0	699	14	CG688262	c 306	15.4	77.0	393	9	AA209714
C 234	15.8	79.0	704	12	BJ931092	c 307	15.4	77.0	400	14	CF50603
C 235	15.8	79.0	707	13	BW038685	c 308	15.4	77.0	407	10	BR061808
C 236	15.8	79.0	711	14	CH423177	c 309	15.4	77.0	407	13	BY228504
C 237	15.8	79.0	714	14	CA413785	c 310	15.4	77.0	407	13	BY228504
C 238	15.8	79.0	714	28	BH578920	c 311	15.4	77.0	421	14	R49177
C 239	15.8	79.0	716	28	BI941998	c 312	15.4	77.0	428	29	BX189233
C 240	15.8	79.0	722	12	BJ151331	c 313	15.4	77.0	429	9	AA387236
C 241	15.8	79.0	727	12	SC468173	c 314	15.4	77.0	435	14	BE44649
C 242	15.8	79.0	728	10	BB381698	c 315	15.4	77.0	441	9	A013929
C 243	15.8	79.0	736	29	CE417738	c 316	15.4	77.0	449	13	BX113931
C 244	15.8	79.0	738	28	BZ52914	c 317	15.4	77.0	450	14	CD72378
C 245	15.8	79.0	739	12	BG615504	c 318	15.4	77.0	452	9	AA881328
C 246	15.8	79.0	742	28	BH650112	c 319	15.4	77.0	453	28	AQ117433
C 247	15.8	79.0	747	29	CE567553	c 320	15.4	77.0	455	13	BY456723
C 248	15.8	79.0	753	14	CD743096	c 321	15.4	77.0	456	9	A013931
C 249	15.8	79.0	755	14	CT738663	c 322	15.4	77.0	474	10	BF660504
C 250	15.8	79.0	767	14	CB29722	c 323	15.4	77.0	474	10	CF156184
C 251	15.8	79.0	767	28	BH650336	c 324	15.4	77.0	477	14	CF157071
C 252	15.8	79.0	769	28	BH490051	c 325	15.4	77.0	477	14	CF158761
C 253	15.8	79.0	774	28	BI9415182	c 326	15.4	77.0	478	10	BF657849
C 254	15.8	79.0	787	14	CA306138	c 327	15.4	77.0	478	14	CA555095
C 255	15.8	79.0	796	9	AU580875	c 328	15.4	77.0	481	13	BY243831
C 256	15.8	79.0	800	12	BI932916	c 329	15.4	77.0	486	28	BH661806
C 257	15.8	79.0	807	29	CG369334	c 330	15.4	77.0	486	28	CC324548
C 258	15.8	79.0	809	28	BH696645	c 331	15.4	77.0	490	28	CC324548
C 259	15.8	79.0	834	9	AL529131	c 332	15.4	77.0	492	28	CH381812
C 260	15.8	79.0	851	10	BF692242	c 333	15.4	77.0	496	10	AW682703
C 261	15.8	79.0	856	28	BI2447974	c 334	15.4	77.0	510	12	BG524561
C 262	15.8	79.0	863	28	BD0944	c 335	15.4	77.0	515	12	CD91038
C 263	15.8	79.0	865	14	CK291457	c 336	15.4	77.0	530	12	BM403834
C 264	15.8	79.0	872	29	CG369341	c 337	15.4	77.0	530	14	CD290266
C 265	15.8	79.0	878	13	CC38186	c 338	15.4	77.0	531	29	CG427151
C 266	15.8	79.0	901	12	BG622103	c 339	15.4	77.0	534	10	BE408994
C 267	15.8	79.0	913	9	AU520808	c 340	15.4	77.0	536	29	CC794545
C 268	15.8	79.0	921	12	BI95157	c 341	15.4	77.0	542	10	CF155910
C 269	15.8	79.0	925	10	BI181394	c 342	15.4	77.0	555	12	BG520816
C 270	15.8	79.0	938	13	BI328627	c 343	15.4	77.0	556	10	BF427832
C 271	15.8	79.0	966	28	BI328628	c 344	15.4	77.0	565	10	BF427832
C 272	15.8	79.0	979	28	BI08657	c 345	15.4	77.0	569	12	BM813690
C 273	15.8	79.0	1011	13	BI0706318	c 346	15.4	77.0	574	28	AQ524050
C 274	15.8	79.0	1060	9	AL575835	c 347	15.4	77.0	575	10	BE75870
C 275	15.8	79.0	1096	12	BG329874	c 348	15.4	77.0	593	10	BF730492
C 276	15.8	79.0	1101	28	CC206155	c 349	15.4	77.0	594	14	CD311937
C 277	15.8	79.0	1125	10	BI790487	c 350	15.4	77.0	594	14	STrP0691
C 278	15.8	79.0	1201	13	BI365741	c 351	15.4	77.0	600	12	CD311937
C 279	15.8	79.0	1432	29	CG756498	c 352	15.4	77.0	600	12	STrP0691
C 280	15.8	79.0	1481	28	CC237544	c 353	15.4	77.0	606	12	BI989303
C 281	15.8	79.0	1560	12	BI413018	c 354	15.4	77.0	612	29	CE68722
C 282	15.8	79.0	1674	11	AK053226	c 355	15.4	77.0	616	12	BI416184
C 283	15.8	79.0	213	28	BI096598	c 356	15.4	77.0	616	12	BI614122
C 284	15.8	79.0	238	10	BB063490	c 357	15.4	77.0	618	14	CK22692
C 285	15.8	79.0	244	29	CG583573	c 358	15.4	77.0	620	14	CB289435
C 286	15.8	79.0	261	10	BP554085	c 359	15.4	77.0	625	14	AZ632296
C 287	15.8	79.0	263	12	BI032343	c 360	15.4	77.0	629	14	CB036010
C 288	15.8	79.0	270	27	BI0420442	c 361	15.4	77.0	631	12	BI494446
C 289	15.8	79.0	273	29	CG596956	c 362	15.4	77.0	634	28	CC050144
C 290	15.8	79.0	283	9	AS386834	c 363	15.4	77.0	636	29	CE628613
C 291	15.8	79.0	286	12	BI033999	c 364	15.4	77.0	639	12	CG415023
C 292	15.8	79.0	287	10	BB181418	c 365	15.4	77.0	639	12	BG15023
C 293	15.8	79.0	300	10	BB264008	c 366	15.4	77.0	647	13	BI161919
C 294	15.8	79.0	304	10	BB266963	c 367	15.4	77.0	648	14	CB05023
C 295	15.8	79.0	305	10	BB230391	c 368	15.4	77.0	650	11	AK05183
C 296	15.8	79.0	351	10	AW470292	c 369	15.4	77.0	654	28	CC182563

C 370	15.4	77.0	658	29	CG400372	01S0511-1	443	15.2	76.0	263	9	AA506314
C 371	15.4	77.0	658	29	CG427792	01S0577-0	C 444	15.2	76.0	264	9	AV238655
C 372	15.4	77.0	661	10	BF006633	ESTA15131	C 445	15.2	76.0	271	9	AV238655
C 373	15.4	77.0	663	28	BH592999	BONU559TR	C 446	15.2	76.0	277	10	BB010692
C 374	15.4	77.0	669	12	BJ389950	BJ389950	C 447	15.2	76.0	286	10	BB242695
C 375	15.4	77.0	671	28	BH765743	BMBAC357C	C 448	15.2	76.0	290	9	AL640424
C 376	15.4	77.0	677	9	AAS56716	Lob10	C 449	15.2	76.0	290	13	BX70974
C 377	15.4	77.0	678	10	BS7790846		C 450	15.2	76.0	293	10	BB005204
C 378	15.4	77.0	680	10	BB357252	BB357252	C 451	15.2	76.0	293	12	BB657032
C 379	15.4	77.0	687	28	BZ495354	BONT135TF	C 452	15.2	76.0	295	14	N78343
C 380	15.4	77.0	690	14	CF997829	VTA019F07	C 453	15.2	76.0	300	9	AV210173
C 381	15.4	77.0	695	14	CD003924		C 454	15.2	76.0	303	9	A1775359
C 382	15.4	77.0	711	28	BH085732	RPT1-24-9	C 455	15.2	76.0	304	10	BB219213
C 383	15.4	77.0	712	12	BS523196		C 456	15.2	76.0	310	10	BB205429
C 384	15.4	77.0	728	28	AQ345909	RPT11-12	C 457	15.2	76.0	311	28	AC04440
C 385	15.4	77.0	765	14	CB323241	UI-MEXO-	C 458	15.2	76.0	318	10	AW902881
C 386	15.4	77.0	782	12	BE6468157	602509732	C 459	15.2	76.0	318	10	BE839446
C 387	15.4	77.0	835	28	BH593136	BOHR037TP	C 460	15.2	76.0	326	12	BG54416
C 388	15.4	77.0	838	29	CNS02014		C 461	15.2	76.0	331	9	AA650522
C 389	15.4	77.0	840	29	CNS05502		C 462	15.2	76.0	334	10	BB22305
C 390	15.4	77.0	843	29	CC520902	CH240-368	C 463	15.2	76.0	342	29	CG98415
C 391	15.4	77.0	843	29	CNS04KIR		C 464	15.2	76.0	344	14	CF506812
C 392	15.4	77.0	846	12	BE719954		C 465	15.2	76.0	354	10	BF2597
C 393	15.4	77.0	848	14	CA985599	CCIX66a23	C 471	15.2	76.0	354	29	CE815638
C 394	15.4	77.0	849	29	CNS04TC5		C 473	15.2	76.0	358	28	AQ010566
C 395	15.4	77.0	857	13	BUS58356	AGENCOURT	C 468	15.2	76.0	363	10	BE655876
C 396	15.4	77.0	857	29	CC805334	2MMBGc047	C 470	15.2	76.0	363	13	CG28415
C 397	15.4	77.0	862	29	CC579888		C 476	15.2	76.0	366	28	MBE979TF
C 398	15.4	77.0	863	29	CG02998	ZMMBG055	C 477	15.2	76.0	367	10	AW447338
C 399	15.4	77.0	864	14	CF823949	UCRCR011	C 478	15.2	76.0	374	14	CD195151
C 400	15.4	77.0	870	29	CC517833	CH240-364	C 479	15.2	76.0	377	13	BY16002
C 401	15.4	77.0	873	29	CG954789	MBED02TR	C 474	15.2	76.0	379	28	AW490991
C 402	15.4	77.0	887	12	BU3300625	HVSME001	C 475	15.2	76.0	380	28	AQ049765
C 403	15.4	77.0	889	13	BX845255	BX845255	C 482	15.2	76.0	387	10	AW542363
C 404	15.4	77.0	896	14	CB560879	AGENCOURT	C 477	15.2	76.0	390	13	BY444993
C 405	15.4	77.0	912	29	CG96743	MBLN56TF	C 483	15.2	76.0	392	10	AN697635
C 406	15.4	77.0	922	13	BG737035		C 479	15.2	76.0	395	28	AQ547841
C 407	15.4	77.0	922	13	BY746278		C 480	15.2	76.0	399	28	AT0673057
C 408	15.4	77.0	952	13	BX341013		C 481	15.2	76.0	404	14	CB811908
C 409	15.4	77.0	980	29	CNS02ZTF		C 482	15.2	76.0	404	10	BF58993
C 410	15.4	77.0	986	29	CG900580	ZMMBB050	C 483	15.2	76.0	411	10	AM343233
C 411	15.4	77.0	1031	12	BI834473	603084638	C 484	15.2	76.0	411	13	BY006359
C 412	15.4	77.0	1201	9	AL513771	AL513771	C 485	15.2	76.0	414	14	CD012333
C 413	15.4	77.0	1201	11	AL564116	AL564116	C 486	15.2	76.0	420	14	AQ0205240
C 414	15.4	77.0	1348	12	BM047112	603621450	C 487	15.2	76.0	421	28	AQ891341
C 415	15.4	77.0	1548	11	AK047418	MUB mubcu	C 488	15.2	76.0	422	14	CP372888
C 416	15.4	77.0	1970	11	AK089011	AK089011	C 489	15.2	76.0	422	14	T90278 yd42008-81
C 417	15.4	77.0	2446	11	AK088533	Mub muscu	C 490	15.2	76.0	429	10	AW484023
C 418	15.4	77.0	2453	11	AK044408	Mub muscu	C 491	15.2	76.0	430	29	CC959567
C 419	15.4	77.0	3254	11	AK054548	Mub muscu	C 492	15.2	76.0	431	10	AD205240 HS 3224
C 420	15.4	77.0	3454	11	AK047026	MUB mubcu	C 493	15.2	76.0	431	10	BB848002
C 421	15.4	77.0	3491	11	AK050673	Mub muscu	C 494	15.2	76.0	434	14	CD195134
C 422	15.4	77.0	3520	11	AK036637	Mub muscu	C 495	15.2	76.0	436	10	BB849928
C 423	15.4	77.0	3812	11	AK034000	Mub muscu	C 496	15.2	76.0	436	14	CB230886
C 424	15.4	77.0	425	12	BI524648	603051625	C 497	15.2	76.0	438	9	A1601572
C 425	15.4	77.0	136	28	BB613777	KBR143C0	C 498	15.2	76.0	439	10	BB6226665
C 426	15.4	77.0	163	29	CE605068		C 499	15.2	76.0	443	9	AI580295
C 427	15.4	77.0	193	28	AZ327421	IM050A16	C 500	15.2	76.0	443	9	A1601294
C 428	15.4	77.0	212	10	BB133381	BB133381	C 501	15.2	76.0	446	10	BB776107
C 429	15.4	77.0	225	29	CB272099	tigr-g98-	C 502	15.2	76.0	450	12	BJ37879
C 430	15.4	77.0	243	13	BK779126		C 503	15.2	76.0	451	9	A1602508
C 431	15.4	77.0	249	9	AL888947	AL888947	C 504	15.2	76.0	451	28	BB6226665
C 432	15.4	77.0	250	9	AV274759		C 505	15.2	76.0	453	10	AI58025 tm403.x
C 433	15.4	77.0	250	9	AV352848		C 506	15.2	76.0	454	10	AW984583
C 434	15.4	77.0	251	12	AK216715	BB8216715	C 507	15.2	76.0	456	10	BB776107
C 435	15.4	77.0	253	10	BB219461	BB219461	C 508	15.2	76.0	457	9	AA17695 o15d10.8
C 436	15.4	77.0	260	23	AV299150	AV299150	C 509	15.2	76.0	458	10	AW64875
C 437	15.4	77.0	266	9	AV293556	AV293556	C 510	15.2	76.0	460	460	AQ801159 HS 3181_A
C 438	15.4	77.0	266	9	AV293556	AV293556	C 511	15.2	76.0	462	13	BB57111 Ba747e05
C 439	15.4	77.0	266	9	AV293556	AV293556	C 512	15.2	76.0	463	28	BB2825560
C 440	15.4	77.0	266	12	BM116138	L0860106-	C 513	15.2	76.0	464	9	AU77638 AU175638
C 441	15.4	77.0	261	12	AV252157	AV252157	C 514	15.2	76.0	469	9	AL889531
C 442	15.4	77.0	261	13	BU896780	X045F03	C 515	15.2	76.0	471	12	BM117916

516	15.2	76.0	472	9	A1189543	c	589	15.2	76.0	574	10	BE35681	
517	15.2	76.0	472	9	A1838722	c	590	15.2	76.0	575	28	A2838089	
c	518	15.2	76.0	472	A066554	c	591	15.2	76.0	576	12	BG895427	
519	15.2	76.0	474	10	sheared_D	c	592	15.2	76.0	578	10	da4dc100B.	
520	15.2	76.0	475	14	CB005274	c	593	15.2	76.0	579	12	AN128767	
521	15.2	76.0	477	9	A1935668	c	594	15.2	76.0	579	12	UI-H-B11-	
522	15.2	76.0	478	12	BI322592	c	595	15.2	76.0	579	29	BJ359158	
523	15.2	76.0	478	13	BX335970	c	596	15.2	76.0	580	13	BJ359316	
c	524	15.2	76.0	479	10	BB114484	c	597	15.2	76.0	581	14	CER62130
c	525	15.2	76.0	481	28	BR2290	c	598	15.2	76.0	583	10	BU721050
c	526	15.2	76.0	489	9	AAB59269	c	599	15.2	76.0	586	12	CB916619
c	527	15.2	76.0	494	9	A1531862	c	600	15.2	76.0	586	14	BF694232
c	528	15.2	76.0	496	13	BQ556161	c	601	15.2	76.0	587	12	BJ361629
c	529	15.2	76.0	497	28	AQ833959	c	602	15.2	76.0	588	14	CC46857
c	530	15.2	76.0	498	12	BQ388628	c	603	15.2	76.0	591	10	CC46857
c	531	15.2	76.0	499	14	W20132	c	604	15.2	76.0	591	14	CA367755
c	532	15.2	76.0	504	12	BQ363161	c	605	15.2	76.0	591	14	CA04168
c	533	15.2	76.0	504	14	CA20521	c	606	15.2	76.0	591	14	BL01N0513
c	534	15.2	76.0	506	28	AQ243748	c	607	15.2	76.0	592	12	BU327803
c	535	15.2	76.0	507	9	A1057550	c	608	15.2	76.0	593	29	CC742217
c	536	15.2	76.0	509	9	AA831831	c	609	15.2	76.0	594	14	W2D111G
c	537	15.2	76.0	509	28	AQ776625	c	610	15.2	76.0	595	14	CA387084
c	538	15.2	76.0	510	14	CB424865	c	611	15.2	76.0	596	13	CB425375
c	539	15.2	76.0	510	14	CF40237	c	612	15.2	76.0	597	19	CD645949
c	540	15.2	76.0	511	12	BQ363045	c	613	15.2	76.0	598	12	BU382256
c	541	15.2	76.0	519	28	AD050167	c	614	15.2	76.0	599	14	BB389256
c	542	15.2	76.0	520	13	BQ809199	c	615	15.2	76.0	600	14	CB916619
c	543	15.2	76.0	520	14	CA545244	c	616	15.2	76.0	600	14	CF486121
c	544	15.2	76.0	520	14	CBT15589	c	617	15.2	76.0	601	12	CF486121
c	545	15.2	76.0	523	28	BH11649	c	618	15.2	76.0	607	14	CD645949
c	546	15.2	76.0	524	12	BM256385	c	619	15.2	76.0	609	28	BB467408
c	547	15.2	76.0	525	14	CB720171	c	620	15.2	76.0	609	9	CD742217
c	548	15.2	76.0	525	28	AQ94449	c	621	15.2	76.0	609	13	DR4C19S
c	549	15.2	76.0	526	28	CC064938	c	622	15.2	76.0	609	13	DU1_35_G
c	550	15.2	76.0	529	10	AW690744	c	623	15.2	76.0	610	12	EB467408
c	551	15.2	76.0	530	14	AD55837	c	624	15.2	76.0	615	9	AW04396
c	552	15.2	76.0	534	12	CH545539	c	625	15.2	76.0	615	12	AU062055
c	553	15.2	76.0	535	29	CG925610	c	626	15.2	76.0	617	13	BB708259
c	554	15.2	76.0	536	14	CA741071	c	627	15.2	76.0	617	13	CB742217
c	555	15.2	76.0	537	10	BE749525	c	628	15.2	76.0	619	28	CD742217
c	556	15.2	76.0	540	28	BH015619	c	629	15.2	76.0	621	12	DU1_35_G
c	557	15.2	76.0	542	10	AW237816	c	630	15.2	76.0	621	14	EB467408
c	558	15.2	76.0	542	10	BB015099	c	631	15.2	76.0	621	12	EB467408
c	559	15.2	76.0	546	12	BI501358	c	632	15.2	76.0	625	13	DU1_35_G
c	560	15.2	76.0	546	12	BM068107	c	633	15.2	76.0	626	13	DU1_35_G
c	561	15.2	76.0	547	10	AW792048	c	634	15.2	76.0	627	12	DU1_35_G
c	562	15.2	76.0	548	9	A1813671	c	635	15.2	76.0	628	12	DU1_35_G
c	563	15.2	76.0	549	14	CD85887	c	636	15.2	76.0	629	28	DU1_35_G
c	564	15.2	76.0	549	28	AQ992197	c	637	15.2	76.0	630	14	DU1_35_G
c	565	15.2	76.0	550	9	A193481	c	638	15.2	76.0	633	13	DU1_35_G
c	566	15.2	76.0	550	14	A193481	c	639	15.2	76.0	633	13	DU1_35_G
c	567	15.2	76.0	550	14	CD649519	c	640	15.2	76.0	634	28	DU1_35_G
c	568	15.2	76.0	551	12	BI382293	c	641	15.2	76.0	634	28	DU1_35_G
c	569	15.2	76.0	551	12	BI359641	c	642	15.2	76.0	635	10	DU1_35_G
c	570	15.2	76.0	553	10	AW55197	c	643	15.2	76.0	635	12	DU1_35_G
c	571	15.2	76.0	554	14	CF162722	c	644	15.2	76.0	640	10	DU1_35_G
c	572	15.2	76.0	555	14	CD613545	c	645	15.2	76.0	640	10	DU1_35_G
c	573	15.2	76.0	555	28	BZ708270	c	646	15.2	76.0	640	28	DU1_35_G
c	574	15.2	76.0	557	29	CG971340	c	647	15.2	76.0	643	12	DU1_35_G
c	575	15.2	76.0	560	13	BI359645	c	648	15.2	76.0	643	12	DU1_35_G
c	576	15.2	76.0	561	28	AZ054783	c	649	15.2	76.0	643	28	DU1_35_G
c	577	15.2	76.0	563	9	A1058278	c	650	15.2	76.0	647	28	DU1_35_G
c	578	15.2	76.0	564	14	CD731776	c	651	15.2	76.0	647	29	DU1_35_G
c	579	15.2	76.0	564	14	CD731776	c	652	15.2	76.0	650	13	DU1_35_G
c	580	15.2	76.0	565	12	BI964009	c	653	15.2	76.0	650	13	DU1_35_G
c	581	15.2	76.0	566	14	CB098319	c	654	15.2	76.0	650	13	DU1_35_G
c	582	15.2	76.0	569	10	BB475053	c	655	15.2	76.0	653	14	DU1_35_G
c	583	15.2	76.0	569	13	BW291970	c	656	15.2	76.0	657	10	DU1_35_G
c	584	15.2	76.0	569	29	CE8219201	c	657	15.2	76.0	658	13	DU1_35_G
c	585	15.2	76.0	571	14	CB825254	c	658	15.2	76.0	659	10	DU1_35_G
c	586	15.2	76.0	572	29	CE694107	c	659	15.2	76.0	660	13	DU1_35_G
c	587	15.2	76.0	573	10	AW474485	c	660	15.2	76.0	661	29	DU1_35_G
c	588	15.2	76.0	573	29	AG231466	c	661	15.2	76.0	662	14	CD719814

C	663	15.2	76.0	666	28	BH2655692	CH230-66G	C	735	15.2	76.0	755	13	BH314869
C	663	15.2	76.0	667	13	B064331	C118C11.	C	736	15.2	76.0	757	12	BH68390
C	665	15.2	76.0	667	28	CD171515	VWB08D02	C	737	15.2	76.0	757	28	CC429570
C	665	15.2	76.0	667	28	B2448557	B244897	C	738	15.2	76.0	758	13	BQ794261
C	666	15.2	76.0	668	12	BW104881	BW104581	C	739	15.2	76.0	759	14	CB28529
C	667	15.2	76.0	669	29	AL711567	DKRZ0861	C	740	15.2	76.0	761	14	CB33845
C	668	15.2	76.0	669	29	CC548342	CH240-432	C	741	15.2	76.0	762	14	CD648590
C	669	15.2	76.0	669	29	CG316817	O3GW1753TH	C	742	15.2	76.0	770	29	CC610038
C	670	15.2	76.0	670	13	BY753784	BY753784	C	743	15.2	76.0	771	28	CC136646
C	671	15.2	76.0	671	29	CG17905	PUIJR83TB	C	744	15.2	76.0	771	29	CG955465
C	672	15.2	76.0	672	14	CF913381	A0646B07-	C	745	15.2	76.0	774	29	CG955297
C	673	15.2	76.0	673	15.2	CE08127	t1gT-q8s-	C	746	15.2	76.0	775	14	CB28506
C	674	15.2	76.0	674	12	BU195501	HWSMEM02	C	747	15.2	76.0	777	12	BI66180
C	675	15.2	76.0	675	12	BI1310778	ESTP31252	C	748	15.2	76.0	777	14	CF318202
C	676	15.2	76.0	676	13	BX275835	CH230-104	C	749	15.2	76.0	782	29	CG881188
C	677	15.2	76.0	677	29	BG91533	NBBR88TF	C	750	15.2	76.0	785	28	BH026368
C	678	15.2	76.0	678	13	BU417073	603670803	C	751	15.2	76.0	786	28	RCI1-24-3
C	679	15.2	76.0	679	14	CE08127	UI-CP-EC1	C	752	15.2	76.0	786	14	BT-R-F506
C	680	15.2	76.0	680	13	BU621226	UI-H-FL1-	C	753	15.2	76.0	787	13	BU164970
C	681	15.2	76.0	681	13	BX275836	BX275836	C	754	15.2	76.0	788	12	BG24583
C	682	15.2	76.0	682	13	BI91372	ESTP51261	C	755	15.2	76.0	789	13	BT77525
C	683	15.2	76.0	683	28	B2659608	O3GAMS69TC	C	756	15.2	76.0	790	29	CG681188
C	684	15.2	76.0	684	14	CA852105	E03C01_C0	C	757	15.2	76.0	793	11	AK006524
C	685	15.2	76.0	685	12	BM971539	UI-CP-EC1	C	758	15.2	76.0	794	11	AK006524
C	686	15.2	76.0	686	14	CB975340	CAB3006_-	C	759	15.2	76.0	795	13	BU110627
C	687	15.2	76.0	687	13	BX845767	BX845767	C	760	15.2	76.0	798	14	CB892947
C	688	15.2	76.0	688	13	AG09884	Pan_trogl	C	761	15.2	76.0	798	13	BT273085
C	689	15.2	76.0	689	12	BP009613	BP009613	C	762	15.2	76.0	799	29	CG100284
C	690	15.2	76.0	690	28	BZ805874	PUGA54TD	C	763	15.2	76.0	800	14	CF532668
C	691	15.2	76.0	691	13	BY750549	BY750549	C	764	15.2	76.0	801	29	CC49320
C	692	15.2	76.0	692	9	AU395348	AU395348	C	765	15.2	76.0	803	29	CG837282
C	693	15.2	76.0	693	15.2	CG896016	pasbac00	C	766	15.2	76.0	804	28	CC076830
C	694	15.2	76.0	694	10	CD273085	60114721	C	767	15.2	76.0	804	29	CG690000
C	695	15.2	76.0	695	12	BM018151	60365747	C	768	15.2	76.0	812	14	CD48583
C	696	15.2	76.0	696	9	AV704562	AV704562	C	769	15.2	76.0	813	14	CD764178
C	697	15.2	76.0	697	10	AZ045328	nweb051D	C	770	15.2	76.0	813	28	CD721719
C	698	15.2	76.0	698	13	BU458089	60374375	C	771	15.2	76.0	814	13	BU133583
C	699	15.2	76.0	699	12	AQ272004	nbx0027G	C	772	15.2	76.0	814	14	CF291300
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C	701	15.2	76.0	701	10	BR020211	BR020211	C	774	15.2	76.0	815	12	BUT26558
C	702	15.2	76.0	702	9	CA419738	UW62e02.x	C	775	15.2	76.0	815	14	CB559013
C	703	15.2	76.0	703	14	CA500469	WHE4020_A	C	776	15.2	76.0	815	14	CA06524
C	704	15.2	76.0	704	13	BUH95470	od166c10.	C	777	15.2	76.0	816	10	BU410227
C	705	15.2	76.0	705	14	CB940620	TPCGU1x4	C	778	15.2	76.0	817	14	CB9415085
C	706	15.2	76.0	706	12	CD405274	Gm_G2854	C	779	15.2	76.0	818	14	CD40583
C	707	15.2	76.0	707	14	CF520295	AGENCOURT	C	780	15.2	76.0	819	13	CD764178
C	708	15.2	76.0	708	14	BH089729	RPT1-24-3	C	781	15.2	76.0	820	12	BT273085
C	709	15.2	76.0	709	14	CH309130	CH230-19-3	C	782	15.2	76.0	821	13	BU133583
C	710	15.2	76.0	710	12	BI1933375	EST53264	C	783	15.2	76.0	822	10	BU622141
C	711	15.2	76.0	711	14	CD650410	CVG10111	C	784	15.2	76.0	822	10	BB515008
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C	716	15.2	76.0	716	14	CF347397	CF347397	C	789	15.2	76.0	828	12	BB131365
C	717	15.2	76.0	717	14	CG999064	ZMBBF052	C	790	15.2	76.0	830	14	BB131365
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C	719	15.2	76.0	719	14	CF536611	UIT-M-G10-	C	792	15.2	76.0	833	29	CG681188
C	720	15.2	76.0	720	28	AZ087043	RPT1-23-6	C	793	15.2	76.0	834	14	CK092088
C	721	15.2	76.0	721	12	BI93121	EST51210	C	794	15.2	76.0	835	12	BI257143
C	722	15.2	76.0	722	14	BU112932	603130703	C	795	15.2	76.0	836	14	BI257143
C	723	15.2	76.0	723	29	CG688654	ZMBBF052	C	796	15.2	76.0	837	14	BI257143
C	724	15.2	76.0	724	13	BO509810	EST617225	C	797	15.2	76.0	838	14	BI257143
C	725	15.2	76.0	725	14	CF22212	SCVFP1304	C	798	15.2	76.0	839	14	BI257143
C	726	15.2	76.0	726	14	CF182433	UIT-M-EYO-	C	799	15.2	76.0	840	13	BI257143
C	727	15.2	76.0	727	14	CB973007	CAB30002_-	C	800	15.2	76.0	841	13	BI257143
C	728	15.2	76.0	728	29	AQ269606	HS23036_B	C	801	15.2	76.0	842	13	BI257143
C	729	15.2	76.0	729	13	BH317037	CH230-120	C	802	15.2	76.0	843	13	BI257143
C	730	15.2	76.0	730	28	BB284374	CH240-205	C	803	15.2	76.0	844	13	BI257143
C	731	15.2	76.0	731	10	BB615375	BB615375	C	804	15.2	76.0	845	13	BI257143
C	732	15.2	76.0	732	28	BB317037	CH230-120	C	805	15.2	76.0	846	13	BI257143
C	733	15.2	76.0	733	29	CC219593	060104ba	C	806	15.2	76.0	847	13	BI257143
C	734	15.2	76.0	734	10	BE393034	BE393034	C	807	15.2	76.0	848	13	BI257143



## ORIGIN

		Db	149 GGTCCATACTCATGTTGATG 130
Query Match	100.0%; Score 20; DB 12; Length 352;		
Best Local Similarity	100.0%; Pred. No. 68; Mismatches 0; Indels 0; Gaps 0;		
Matches	20; Conservative		
Oy	1 GGTCCATACTCATGTTGATG 20		
Db	283 GGTCCATACTCATGTTGATG 302		
RESULT 4	CB852193/c		
LOCUS	CB852193	359 bp	mRNA linear EST 22-APR-2003
DEFINITION	UI-CF-FNO-aeg-1-02-0-UI-s1 UI-CF-FNO Homo sapiens cDNA clone		
ACCESSION	CB852193	370 bp	mRNA linear EST 05-MAR-2002
VERSION	CB852193.1	302	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 359)		
AUTHORS	Bonaldo, M.P., Lennon, G. and Soares, M.B.		
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery		
JOURNAL	Genome Res. 6 (9), 791-806 (1996)		
MEDLINE	97044477		
PUBMED	8883548		
COMMENT	Contact: McCray, PB		
McCravy Lab			
University of Iowa			
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA			
TeL:	319 356 4866		
Fax:	319 356 7171		
Email:	paul-mccravy@uiowa.edu		
Tissue Procurement:	Dr. M. J. Welsh, University of Iowa		
cDNA Library Preparation:	Dr. M. Bento Soares, University of Iowa		
CDNA Library Arrayed by:	Dr. M. Bento Soares, University of Iowa		
DN A Sequencing by:	Dr. M. Bento Soares, University of Iowa		
DNA Distribution:	Researchers may obtain clones from Research Genetics ( <a href="http://www.resgen.com">www.resgen.com</a> )		
The following repetitive elements were found in this cDNA sequence:	249-275, >AT rich< low complexity (matched complement) Seq primer: M13 FORWARD POLY(A)-No.		
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Location/Qualifiers			
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ORIGIN			
Query Match	100.0%; Score 20; DB 12; Length 370;		
Best Local Similarity	100.0%; Pred. No. 70; Mismatches 0; Indels 0; Gaps 0;		
Matches	20; Conservative		
Oy	1 GGTCCATACTCATGTTGATG 20		
Db	121 GGTCCATACTCATGTTGATG 102		
RESULT 6	AV687532/c		
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DEFINITION	AV687532 GKC Homo sapiens cDNA clone GKCDCA01 5', mRNA sequence.		
ACCESSION	AV687532		
VERSION	AV687532.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
Query Match	100.0%; Score 20; DB 14; Length 359;		
Best Local Similarity	100.0%; Pred. No. 69; Mismatches 0; Indels 0; Gaps 0;		
Matches	20; Conservative		
Oy	1 GGTCGATCTCATGTTGATG 20		



Qy	1	GTCCTACTATGTTGATG	20		RESULT 9	BU679004	BU679004	100.0%; Score 20; DB 9; Length 437; Best Local Similarity 100.0%; Pred. No. 75; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ORIGIN
Db	158	GGTCCATACTATGTTGATG	177						
Qy	1	GTCCTACTATGTTGATG	20		RESULT 10	AA828925	AA828925	100.0%; Score 20; DB 13; Length 461; Best Local Similarity 100.0%; Pred. No. 77; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ORIGIN
Db	175	GGTCCATACTATGTTGATG	194						
FEATURES					DEFINITION	AA828925	AA828925	486 bp mRNA linear EST 07-APR-1998	DEFINITION
SOURCES					LOCUS	AA828925	AA828925	AA828925	LOCUS
					DEFINITION	AA828925	AA828925	AA828925	DEFINITION
					ORGANISM	AA828925	AA828925	AA828925	ORGANISM
					AUTHORS	AA828925	AA828925	AA828925	AUTHORS
					TITLE	AA828925	AA828925	AA828925	TITLE
					COMMENT	AA828925	AA828925	AA828925	COMMENT
					CONTACT	AA828925	AA828925	AA828925	CONTACT
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					University of Iowa	AA828925	AA828925	AA828925	University of Iowa
					2024 University of Iowa Med Labs, Iowa City, IA 52242, USA	AA828925	AA828925	AA828925	2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
					Te: 319 356 4866	AA828925	AA828925	AA828925	Te: 319 356 4866
					Fax: 319 356 7171	AA828925	AA828925	AA828925	Fax: 319 356 7171
					Email: paul-mccrory@uiowa.edu	AA828925	AA828925	AA828925	Email: paul-mccrory@uiowa.edu
					Tissue Procurement: Dr. M. J. Welsh, University of Iowa	AA828925	AA828925	AA828925	Tissue Procurement: Dr. M. J. Welsh, University of Iowa
					cDNA Library preparation: Dr. M. Bento Soares, University of Iowa	AA828925	AA828925	AA828925	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
					DNA Sequencing by: Dr. M. Bento Soares, University of Iowa	AA828925	AA828925	AA828925	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
					Clone Distribution: Researchers may obtain clones from Research	AA828925	AA828925	AA828925	Clone Distribution: Researchers may obtain clones from Research
					Genetics ( <a href="http://www.resgen.com">www.resgen.com</a> ) or from Open Biosystems ( <a href="http://www.openbiosystems.com">www.openbiosystems.com</a> )	AA828925	AA828925	AA828925	Genetics ( <a href="http://www.resgen.com">www.resgen.com</a> ) or from Open Biosystems ( <a href="http://www.openbiosystems.com">www.openbiosystems.com</a> )
					The following repetitive elements were found in this cDNA	AA828925	AA828925	AA828925	The following repetitive elements were found in this cDNA
					Sequence: 49-75, >AT-rich#Low_complexity (matched complement)	AA828925	AA828925	AA828925	Sequence: 49-75, >AT-rich#Low_complexity (matched complement)
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					FEATURES	AA828925	AA828925	AA828925	FEATURES
					SOURCES	AA828925	AA828925	AA828925	SOURCES
					Location/Qualifiers	AA828925	AA828925	AA828925	Location/Qualifiers
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					/mol_type="mRNA"	AA828925	AA828925	AA828925	/mol_type="mRNA"
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					/clone="UI-CF-DU1-aat-o-05-0-UI"	AA828925	AA828925	AA828925	/clone="UI-CF-DU1-aat-o-05-0-UI"
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					/dev_stage="Adult"	AA828925	AA828925	AA828925	/dev_stage="Adult"
					/lab_host="DH10B (Life Technologies) (T1 phage resistant)"	AA828925	AA828925	AA828925	/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
					/clone_lib="UI-CF-DU1"	AA828925	AA828925	AA828925	/clone_lib="UI-CF-DU1"
					/note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;"	AA828925	AA828925	AA828925	/note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;"
					UI-CF-DU1 is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1995. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Eco R I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this	AA828925	AA828925	AA828925	UI-CF-DU1 is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1995. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Eco R I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
					library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this	AA828925	AA828925	AA828925	library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
					library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this	AA828925	AA828925	AA828925	library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
					GENE	AA828925	AA828925	AA828925	GENE
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					Best Local Similarity	AA828925	AA828925	AA828925	Best Local Similarity
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					0;匹配	AA828925	AA828925	AA828925	0;匹配
					0;保守性	AA828925	AA828925	AA828925	0;保守性
					0;差异	AA828925	AA828925	AA828925	0;差异
					0;插入	AA828925	AA828925	AA828925	0;插入
					0;删除	AA828925	AA828925	AA828925	0;删除
					0;缺口	AA828925	AA828925	AA828925	0;缺口
					0;匹配	AA828925	AA828925	AA828925	0;匹配
					0;保守性	AA828925	AA828925	AA828925	0;保守性
					0;差异	AA828925	AA828925	AA828925	0;差异
					0;插入	AA828925	AA828925	AA828925	0;插入
					0;删除	AA828925	AA828925	AA828925	0;删除
					0;缺口	AA828925	AA828925	AA828925	0;缺口
					0;匹配	AA828925	AA828925	AA828925	0;匹配
					0;保守性	AA828925	AA828925	AA828925	0;保守性
					0;差异	AA828925	AA828925	AA828925	0;差异
					0;插入	AA828925	AA828925	AA828925	0;插入
					0;删除	AA828925	AA828925	AA828925	0;删除
					0;缺口	AA828925	AA828925	AA828925	0;缺口
					0;匹配	AA828925	AA828925	AA828925	0;匹配
					0;保守性	AA828925	AA828925	AA828925	0;保守性
					0;差异	AA828925	AA828925	AA828925	0;差异
					0;插入	AA828925	AA828925	AA828925	0;插入
					0;删除	AA828925	AA828925	AA828925	0;删除
					0;缺口	AA828925	AA828925	AA828925	0;缺口
					0;匹配	AA828925	AA828925	AA828925	0;匹配
					0;保守性	AA828925	AA828925	AA828925	0;保守性
					0;差异	AA828925	AA828925	AA828925	0;差异
					0;插入	AA828925	AA828925	AA828925	0;插入
					0;删除	AA828925	AA828925	AA828925	0;删除
					0;缺口	AA828925	AA828925	AA828925	0;缺口
					0;匹配	AA828925	AA828925	AA828925	0;匹配
					0;保守性	AA828925	AA828925	AA828925	0;保守性

DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS ;, mRNA sequence.

ACCESSION B1793276  
VERSION B1793276.1 GI:15821001  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 487)

AUTHORS Melton,D., Brown,J., Kent,G., Permutt,A., Lee,C., Kaestner,K.,  
Lemishka,I., Searce,M., Brastein,J., Gradowohl,G., Clifton,S.,  
Hillier,L., Marra,M., Papo,D., Wylie,T., Martin,J., Blisbain,A.,  
Schmitt,A., Theising,B., Ritter,E., Ronko,T., Bennett,J.,  
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,  
Williams,T., Jackson,Y. and Bowers,Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)

TITLE Other ESTs: J:50b09, x1  
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biolab.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Juliana Brown  
(brown@fas.harvard.edu) This sequence now available from the IMAGE  
Seq primer: -40RP from Gibco  
High quality sequence stop: 261.

FEATURES source  
1. . 487  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5670113"  
/sex="Both"  
/tissue\_type="Islets of Langerhans"  
/dev\_stage="Adult"  
/lab\_host="DRI:OB"  
/clone lib="Melton Normalized Human Islet 4 N4-HITS 1"  
/note="Organ: Pancreas; Vector: pSPORT1; Site\_1: Not 1;  
Site\_2: Sal 1; Starting library constructed using  
SuperScript Plasmid Library kit (Life Technologies). CDNA  
made by oligo-dT priming. Size-selected by column  
fractionation; average insert size 1.08 kb. Library was  
amplified once on solid support and plasmid DNA from  
library was prepared. The library DNA was normalized by  
method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
Research 6:791-806; 0.5 microgram single-stranded library  
plasmid DNA was mixed with 5 micromgals PCR product  
representing library inserts and hybridized to an EcoI of  
representing library. 5' hydroxylated (unhybridized) plasmids were isolated  
by hydroxyapatite chromatography and used to make this  
library."

ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 487;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 20; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTTGATG 20  
Db 246 GGTCCATACTCATGTTGATG 227

RESULT 13  
BQ186624/c BQ186624  
LOCUS BQ186624 510 bp mRNA linear EST 30-APR-2002  
DEFINITION UI-B-EJ1-ajr-n-03-0-UI.r1 UI-EJ1 Homo sapiens cDNA clone  
UI-B-EJ1-ajr-n-03-0-UI 5', mRNA sequence.

ACCESSION BQ186624  
VERSION BQ186624.1 GI:20362175  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 510)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 9704477  
PUBMED 8889548

COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics ( <a href="http://www.resgen.com">www.resgen.com</a> ). The following repetitive elements were found in this cDNA sequence: 432<458, >AT rich<low_complexity (matched complement) Seq primer: M13 REVERSE Location/Qualifiers
FEATURES	source
1. 510	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-E-EJ1-ajr-n-03-0-UI" /tissue_type="fetal eye, lens, eye anterior segment, optic nerve, retina, RPE and Choroid" /dev_stage="fetal and adult" /lab_host="DHIOB (Life Technologies) (T1 phage resistant)" /clone_lib="UI-E-EJ1" /note="Organ: eye; Vector: pMT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EJ1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated with an EcoR I adaptor, digested with Not I, and cloned directionally into pMT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dR18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATGGGA; eye anterior segment, ATGGCGCAT; optic nerve, CCATTAAGG; retina, CCGGG; Retina Foveal and Macular, GTCG; RPE and Choroid, ACCTA. This library was created for the program and Choroid, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
ORIGIN	
Query Match	100.0%; Score 20; DB 13; Length 510; Best Local Similarity 100.0%; Pred. No. 80; Mismatches 0; Indels 0; Gaps 0;
QY	1 GTGCCATACATGTGTATG 20
Db	332 GGTCCATACATGTGTATG 313
RESULT 14	
AA166911	AA166911 513 bp mRNA linear EST 09-MAR-1998 DEFINITION zip05g10.81 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:95554 3' similar to gb:D4533 DNA-REPAIR PROTEIN ELEMENT ; mRNA sequence.
ACCESSION	COMPLEMENTING XP-A CELLS (HUMAN);contains MER37.t2 MBR37 repetitive element ; mRNA sequence.
VERSION	AA166911.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Mammalia; Etherida; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Homo sapiens
REFERENCE	I (bases 1 to 515) Bonaldo, M.P., Lennon, G. and Soares, M.B.
AUTHORS	Normalization and subtraction: two approaches to facilitate gene discovery
TITLE	Normalizaion and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	97044477
PUBMED	889548
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
COMMENT	Martin,J.; Moore,B.; Scheibenbogen,K.; Steptoe,M.; Tan,F.; Theising,B.; White,Y.; Wyly,T.; Waterston,R. and Wilson,R. Washington University EST Project Unpublished (1997) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LILN; contact the IMAGE Consortium ( <a href="mailto:intc@image.lnl.gov">intc@image.lnl.gov</a> ) for further information. Insert Length: 667 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 263.
FEATURES	source
1. 513	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:595554" /sex="female" /dev_stage="adult, 64 years" /lab_host="SOLR (kanamycin resistant)" /clone_lib="stratagene ovarian cancer (#937219)" /note="Vector: Bluescript SK-, Site_1: EcoRI; Site_2: XbaI; Cloned unidirectionally. Primer: Oligo dT. Papillary serous carcinoma, isolated from ascites, 64 year old caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTGGCCGAG 3', ~3' adaptor sequence: 5' CTGAGTTTTRTRTRTRTRTTT 3,"
ORIGIN	
Query Match	100.0%; Score 20; DB 9; Length 513; Best Local Similarity 100.0%; Pred. No. 80; Mismatches 0; Indels 0; Gaps 0;
QY	1 GGTCCATACATGTGTATG 20
Db	357 GGTCCATACATGTGTATG 376
RESULT 15	
BQ184648	BQ184648 515 bp mRNA linear EST 30-APR-2002 DEFINITION UI-E-EJ1-ajr-n-03-0-UI..81 UI-E-EJ1 Homo sapiens cDNA clone
ACCESSION	UI-E-EJ1-ajr-n-03-0-UI 3', mRNA sequence.
VERSION	BQ184648
SOURCE	BQ184648.1 GI:20360199
EST.	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
MEDLINE	
PUBMED	
COMMENT	Contact: Soares, MB Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregg Hageman cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research

Genetics ([www.resgen.com](http://www.resgen.com)). elements were found in this cDNA

The following repetitive sequence: 49-75, >AT rich#Low\_complexity (matched compliment)

Seq primer: M13 FORWARD

POLYA=Yes.

#### FEATURES source Location/Qualifiers

1. q515  
 /organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone\_lib="UI-E-EJ1"

/tissue\_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"

/dev\_stage="fetal and adult"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_lib="UI-E-EJ1"

/note="Organ: eye; Vector: pTT3'-pac (Pharmacia) with a modified polylinker; Site\_1: BCR I; Site\_2: Not I;

UI-E-EJ1 is a subtracted cDNA library constructed

according to Bonaldo, Lemmon and Soares, Genome Research, 6:791-795, 1996. First strand cDNA synthesis was primed with an oligo(dT) primer containing a Not I site. Double stranded cDNA was ligated onto an EcoR I adaptor, digested with Not I, and cloned directionally into pTT3'-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes,

AGANTCAGA; lens, CGATTAGCA; eye anterior segment,

AATGCCGAT; optic nerve, CCATTAAGC; retina, CCGGG; Retina

Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This

library was created for the PRC and Choroid, Gene Discovery in the

Visual System, supported by National Eye Institute (NEI).

TAG TISSUE=Foveal and Macular Retina

TAG LIB=UI-E-EJ1

TAG\_SEQ=GTCC"

#### ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 515;

Best Local Similarity 100.0%; Pred. No. 80;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTGATG 20

Dy 175 GGTCCATACTCATGTGATG 194

#### ORIGIN

Query Match

100.0%; Score 20;

DB 10; Length 534;

Best Local Similarity

100.0%; Pred. No. 82;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTGATG 20

Dy 430 GGTCCATACTCATGTGATG 449

#### RESULT 16

AW890854

AW890854 534 bp mRNA linear EST 24-MAY-2000

LOCUS DEFINITION RCS\_NT0053-100500-021-G11 NT0053 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW890854

VERSION AW890854.1

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)

#### RESULT 17

CB048344/c

LOCUS CB048344

DEFINITION NISC\_9704c05\_Y1 NCI\_CGAP\_P-28 Homo sapiens cDNA clone IMAGE-2270537

5, mRNA sequence.

CB048344

CB048344.1

EST.

SOURCE

ORGANISM Homo sapiens (human)

#### RESULT 18

AW890854

AW890854 534 bp mRNA linear EST 24-MAY-2000

LOCUS DEFINITION RCS\_NT0053-100500-021-G11 NT0053 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW890854

VERSION AW890854.1

KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)

#### REFERENCE

1 (bases 1 to 587)

#### COMMENT

JOURNAL

Unpublished (1997)

CONTACT

Contact: Robert Strausberg, Ph.D.

COMMENT

#### FEATURES source

CDNA Library Preparation:

The I.M.A.G.E. Consortium/LINL

CDNA Sequencing by:

National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

info@image.llnl.gov

Plate: L1MM006 row: F column: 10

Seq primer: M13RPL reverse primer (ABI).

Location/Qualifiers

1. .587

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMGR:3270537"

/sex="male"

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil Tel: +55-11-2707001

Fax: +55-11-2707001

Email: asimmon@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-NT0053-100500-021-G11&t3=2000-05-10&t4=1>)

Seq primer: puc 18 forward

High quality sequence start: 12

High quality sequence stop: 486.

#### FEATURES source

Query Match

100.0%; Score 20;

DB 10; Length 534;

Best Local Similarity

100.0%; Pred. No. 82;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTGATG 20

Dy 430 GGTCCATACTCATGTGATG 449

#### ORIGIN

Query Match

100.0%; Score 20;

DB 10; Length 534;

Best Local Similarity

100.0%; Pred. No. 82;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTGATG 20

Dy 430 GGTCCATACTCATGTGATG 449

#### RESULT 17

CB048344/c

LOCUS CB048344

DEFINITION NISC\_9704c05\_Y1 NCI\_CGAP\_P-28 Homo sapiens cDNA clone IMAGE-2270537

5, mRNA sequence.

CB048344

CB048344.1

EST.

SOURCE

ORGANISM Homo sapiens (human)

#### REFERENCE

1 (bases 1 to 587)

#### COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgrops@mail.nih.gov

CDNA Library Preparation:

The I.M.A.G.E. Consortium/LINL

CDNA Sequencing by:

National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

info@image.llnl.gov

Plate: L1MM006 row: F column: 10

Seq primer: M13RPL reverse primer (ABI).

Location/Qualifiers

1. .587

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMGR:3270537"

/sex="male"

Laboratory of Cancer Genetics

```

/dev_stage="adult"
/lab-host="DH10B"
/clone-lib="NCI CGAP Pr28"
/note="Organ: prostate; vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI CGAP Pr28 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217926-122615).
Subtraction by Bentto Soares and M. Fatima Bonaldo."

```

	Score	DB	Length	Identity	Pred.	No.	Mismatches	Indels	Gaps
TACTCATGTTGATG	20			100.0%	20	DB 14	587		
TACTCATGTTGATG	195			100.0%	100.0%	Pred. No. 85	0	0	0;
						Mismatches 0;			
						Indels 0;			
						Gaps 0;			

591 bp mRNA linear EST 17-JAN-2003  
 sequence.

.1 GI:27786630

iens (human)

a, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 |; Butheria; Primates; Catarrhini; Hominidae; Homo.  
 | to 591)  
<http://www.ncbi.nlm.nih.gov/ncigap>.

LAM006 row: F column: 10  
 Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 ne Index  
 hed (1997)

Robert Strauberg, Ph.D.  
 gabbs@nmail.nih.gov

ary Preparation:  
 brary Arrayed by: The I.M.A.G.E. Consortium/LNLL  
 uencing by: National Institutes of Health Intramural  
 ng Center (NIISC)  
 istribution: NCI-CGAP Clone distribution information can be  
 rough the I.M.A.G.E. Consortium/LNLL at:  
 ge.LNL.gov  
 LAM006 row: F column: 10  
 er: -21M3 forward primer (ABI).  
 Location/Qualifiers

1. .591

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3205337"  
 /sex="male"

/dev\_stage="adult"  
 /lab-host="DH10B"  
 /clone-lib="NCI CGAP Pr28"  
 /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)  
 with a modified polylinker; Plasmid DNA from the  
 normalized library NCI CGAP Pr28 was prepared, and ss  
 circles were made in vitro. Following HAP purification,  
 this DNA was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from a pool  
 of 5,000 clones made from the same library (cloneIDs  
 985608-986759, 1101192-1101959, and 1217926-122615).  
 Subtraction by Bentto Soares and M. Fatima Bonaldo."

Dy	RESULT 19	Best Local Similarity 100%; Pred. No. 85; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	AW979099	AW979099 592 bp mRNA linear EST 02-JUN-2000
	DEFINITION	MAGE resequences, MAGP
	ACCESSION	EST91209
	VERSION	AW979099
	KEYWORDS	MAGE resequences, MAGP
	SOURCE	Homo sapiens (human)
	ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
	REFERENCE	1 (bases 1 to 592)
	AUTHORS	Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.B., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
	JOURNAL	Unpublished (2000)
	COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnq@tigr.org Plate: 402
	FEATURES	Seq primer: Forward
	source	Location/Qualifiers
		1. . 592
		/organism="Homo sapiens"
		/mol_type="mRNA"
		/db_xref="TAXON:9606"
		/clone_id="MAGE resequences, MAGP"
		/note="Vector: pBluescriptSKm",
	ORIGIN	
	RESULT 20	Query Match 100 %; Score 20; DB 10; Length 592; Best Local Similarity 100%; Pred. No. 85; Mismatches 0; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy	BMT39320	595 bp mRNA linear EST 01-MAR-2002
Db	K-BST0008760	S2SNNU668 Homo sapiens cDNA clone S2SNNU668-6-H08 5', mRNA sequence.
	ACCESSION	BMT39320
	VERSION	BMT39320.1
	KEYWORDS	GTCATCATCTCATGTCATG 20 289
	EST.	
	ORGANISM	Homo sapiens (human)
	SOURCE	Bukeryo, Y.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
	REFERENCE	1 (bases 1 to 595)
	AUTHORS	Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
	TITLE	ZIC Frontier Korean EST Project 2001
	COMMENT	Contract: Kim, Y.S. Unpublished (2002)

52 Boeun-dong Yusong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4710

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 6 row: H column: 08

High quality sequence stop: 595.

#### FEATURES

##### source

Location/Qualifiers  
1. .595  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="52SNU68-6-H08"  
/sex="M"  
/tissue\_type="Ascites"  
/cell\_type="Epithelial"  
/cell\_line="SNU-66B"  
/lab\_host="Top10F"  
/note="Organ: Stomach; Vector: pCNS; Site\_1: EcoRI;  
Site\_2: NotI; The poly(A)+ RNA was decapped with tobacco  
acid pyrophosphatase (TnP) and ligated with DNA-RNA linker  
including EcoRI site by treatment of T4 RNA ligase. The  
first strand cDNA was synthesized from oligo dT-selected  
mRNA by priming with dT-tailed vector. The dT-tailed  
vector was adjusted to have about 60nt. The cDNA vector  
was circularized with E. coli DNA ligase after digestion  
of EcoRI which site is also included in vector. An RNA  
strand converted to a DNA strand by Okayama-Berg method.  
The obtained cDNA vectors were used for transformation of  
competent cells E. coli Top10F' by electroporation  
method."

#### ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 595;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTCCATACTCATGTGATG 20  
Db 412 GGTCCATACTCATGTGATG 393

#### RESULT 21

LOCUS BR'92983 598 bp mRNA linear EST 12-MAR-2002  
DEFINITION Melton Normalized Human Islet 4 N4-H1S 1 Homo sapiens  
VERSION e00b09\_x1  
SOURCE IMAGE:5670113 3, similar to SW\_XPA\_HUMAN F23025  
ACCESSION B1792983  
KEYWORDS DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS ;, mRNA sequence.

VERSION B1792983.1 GI:15820708

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 598)  
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarce,M., Brestelli,J., Gradvohl,G., Clifton,S., Hillier,L., Narra,M., Pape,D., Wyllie,T., Martin,J., Blitsain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cerdas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.

TITLE Unpublished (2000)  
JOURNAL COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA, 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@bio.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing by:

#### FEATURES

##### source

Location/Qualifiers  
1. .598  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5670113"  
/sex="Both"  
/tissue\_type="Islets of Langerhans"  
/lab\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="Melton Normalized Human Islet 4 N4-H1S 1"  
/note="organ: Pancreas; Vector: pSPRT1; Site\_1: Not 1;  
Site\_2: Sal 1; Starting library constructed using  
SuperScript Plasmid Library kit (Life Technologies). cDNA  
made by oligo-dT priming. Size-selected by column  
fractionation; average insert size 1.08 kb. Library was  
amplified once on solid support and plasmid DNA from  
library was prepared. The library DNA was normalized by  
method #4 from Bonaldo, Lennon, and Soares 1996 Genome  
Research 6:791-806; 0.5 microgram single-stranded library  
plasmid DNA was mixed with 5 micrograms PCR product  
representing library inserts and hybridized to an Ecot of  
20. Single-stranded (unhybridized) plasmids were isolated  
by hydroxyapatite chromatography and used to make this  
library."

#### ORIGIN

Query Match 100.0%; Score 20; DB 12; Length 598;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTCCATACTCATGTGATG 20  
Db 354 GGTCCATACTCATGTGATG 373

#### RESULT 22

LOCUS BR446397 627 bp mRNA linear EST 01-DEC-2000  
DEFINITION 7p36905.x1 NCI CGAP P+28 Homo sapiens cDNA clone IMAGE:3648176 3,  
similar to SW\_XPA\_HUMAN P23025 DNA-REPAIR PROTEIN COMPLEMENTING  
XP-A CELLS ; contains MER37.t2 MER37 repetitive element ;, mRNA  
sequence.

VERSION BR446397.1 GI:11511535

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 627)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

COMMENT Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lemon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution by: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. consortium/LNL, send email to:  
info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 460.

**FEATURES**  
 source

 Location/Qualifiers  
 1. 627

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3648176"

/sex="male"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Pr28"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)

with a modified polylinker; Vector: Plasmid DNA from the

normalized library NCI CGAP Pr22 was prepared, and 88

circles were made in vitro. Following RAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNA from a pool

of 5,000 clones made from the same library (cloneIDs

98508-986759, 1101192-1101939, and 1217928-1226151).

Subtraction by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

Query Match

Best Local Similarity

Matches

Score 20;

DB 10;

Length 627;

Pred. No. 87;

Mismatches 0;

Indels 0;

Gaps 0;

OY

1 GGTCCATACTCATGTGTAG 20

Db 69 GGTCCATACTCATGTGTAG 50

## FEATURES

source

Location/Qualifiers

1. 627

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3648176"

/sex="male"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Pr28"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)

with a modified polylinker; Vector: Plasmid DNA from the

normalized library NCI CGAP Pr22 was prepared, and 88

circles were made in vitro. Following RAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNA from a pool

of 5,000 clones made from the same library (cloneIDs

98508-986759, 1101192-1101939, and 1217928-1226151).

Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match

Best Local Similarity

Matches

Score 20;

DB 12;

Length 638;

Pred. No. 88;

Mismatches 0;

Indels 0;

Gaps 0;

OY

1 GGTCCATACTCATGTGTAG 20

Db 619 GGTCCATACTCATGTGTAG 600

Research 6(9): 791-805. RNA was prepared from harvested

cells of SNU-16 culture. SNU-16 cell was obtained from

Korean Cell Line Bank (KCLB). SNU-16 was established from

ascitic fluids of Korean patients by Park J.G. et al.

(1990), Cancer Res 50: 2773-2780."

## ORIGIN

Query Match

Best Local Similarity

Matches

Score 20;

DB 12;

Length 638;

Pred. No. 88;

Mismatches 0;

Indels 0;

Gaps 0;

OY

1 GGTCCATACTCATGTGTAG 20

Db 69 GGTCCATACTCATGTGTAG 50

## FEATURES

source

Location/Qualifiers

1. 627

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5214347"

/tissue\_type="leukocyte"

/lab\_host="DH10B"

/clone\_lib="NIH\_MCC\_118"

/note="Vector: pCMV-SPORT6, Site\_1: NotI; Site\_2: EcoRV

(destroyed); RNA source Leukocytes from anonymous pool of

non-activated adult donors. Library is oligo-dT primed

and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

1.2-3.3 kb. Library is normalized and enriched for

full length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 027. Note:

this is a NIH\_MCC library."

ORIGIN

Query Match

Best Local Similarity

Matches

Score 20;

DB 12;

Length 639;

Pred. No. 88;

Mismatches 0;

Indels 0;

Gaps 0;

OY

1 GGTCCATACTCATGTGTAG 20

Db 619 GGTCCATACTCATGTGTAG 600

RESULT 25  
 CB305774 CB305774 672 bp mRNA linear EST 04-MAR-2003  
 DEFINITION UI-CF-EN1-aeg-k-02-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
 VERSION CB305774.1 GI:28846285  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 672)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 JOURNAL Genome Res. 6 (9), 791-806 (1996)  
 MEDLINE 9704477  
 PUBLMED 8889548  
 COMMENT Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Fax: 319 356 4866  
 Tel: 319 356 4866  
 Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics ([www.resgen.com](http://www.resgen.com)) or from Open Biosystems  
 ([www.openbiosystems.com](http://www.openbiosystems.com)).  
 The following repetitive elements were found in this cDNA  
 sequence: 490-521, >AT rich<low\_complexity (matched compliment).  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES source  
 location/Qualifiers  
 1. .672  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-EN1-aeg-k-02-0-UI"  
 /tissue\_type="Primary Lung Cystic Fibrosis Epithelial  
 Cells"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_id="UI-CF-EN1"  
 /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Bcor 1; Site 2: Not 1;  
 UI-CP-EN1 is a normalized cDNA library containing the  
 following tissue(s): Primary Lung Cystic Fibrosis  
 Epithelial Cells. The library was constructed according to  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. First strand cDNA synthesis was primed with an  
 oligo-dT primer containing a Not 1 site. Double stranded  
 cDNA was ligated to an Bcor 1 adaptor, digested with Not  
 1, and cloned directionally into pT7T3-Pac vector. The  
 oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not 1 site and the (dT)18 tail. The  
 sequence tag for this library is CTGCTCTGGT.  
 TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS  
 6hr to LPS 24h  
 TAG LIB=UI-CF-EN1  
 TAG SEQ=CTGCTCTGGT"

ORIGIN  
 Query Match 100.0%; Score 20; DB 14; Length 672;  
 Best Local Similarity 100.0%; Pred. No. 90; Mismatches 0;  
 Matches 20; Conservative 0; Indels 0; Gaps 0;

Db 621 GTTCATACATGTGATG 640  
 RESULT 26  
 BM92090 BM92090 678 bp mRNA linear EST 17-JUN-2002  
 LOCUS UI-H-DF1-lauf-m-16-0-UI.s1 NCI\_CGAP\_DFI Homo sapiens cDNA clone  
 DEFINITION IMAGE:586855 3', mRNA sequence.  
 ACCESSION BM92090  
 VERSION BM92090.1 GI:19711479  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 678)  
 NCI -CGAP http://www.ncbi.nlm.nih.gov/cgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbsr@mail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
 The following repetitive elements were found in this cDNA  
 sequence: 501-527, >AT rich<low\_complexity (matched compliment).  
 Seq primer: M13 FORWARD  
 POLYA=Yes.  
 location/Qualifiers  
 1. .678  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5868855"  
 /tissue\_type="Subchondral Bone"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_id="NCI\_CGAP\_DFI"  
 /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Bcor 1; Site 2: Not 1;  
 NCI CGAP DFI is a normalized cDNA library containing the  
 following tissue(s): Subchondral Bone. The library was  
 constructed according to Bonaldo, Lennon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not 1 site. Double stranded cDNA was ligated to an Bcor 1  
 adaptor, digested with Not 1, and cloned directionally  
 into pT7T3-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not 1 site and the  
 (dT)18 tail. The sequence tag for this library is  
 GTTAAAGCGTC.  
 TAG TISSUE=subchondral bone  
 TAG LIB=UI-H-DF1  
 TAG SEQ=GTAAAGCGTC"

ORIGIN  
 Query Match 100.0%; Score 20; DB 12; Length 678;  
 Best Local Similarity 100.0%; Pred. No. 90; Mismatches 0;  
 Matches 20; Conservative 0; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTGATG 20  
 Db 627 GGTCCATACTCATGTGATG 646  
 RESULT 27  
 CA450156

**LOCUS** CA450156 705 bp mRNA linear EST 08-NOV-2002  
**DEFINITION** UI-CF-FNO-aff-k-13-0-UI\_B1 UI-CF-FNO Homo sapiens cDNA clone  
**REFERENCE** UT-CF-FNO-aff-k-13-0-UI 3', mRNA sequence.  
**ACCESSION** CA450156  
**VERSION** CA450156.1 GI:24814576  
**SOURCE**  
**ORGANISM** Homo sapiens (human)  
**Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;**  
**Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.**  
**AUTHORS** I (bases 1 to 705);  
**Bonaldo, M.P., Lennon, G. and Soares, M.B.**  
**TITLE** Normalization and subtraction: two approaches to facilitate gene  
**discovery**  
**JOURNAL** Genome Res. 6 (9), 791-806 (1996)  
**MEDLINE** 9704477  
**PUBMED** 8889548  
**COMMENT**  
**CONTACT:** McCray, PB  
**McCracken, Lab**  
**University of Iowa**  
**2024 University of Iowa Med Labs, Iowa City, IA 52242, USA**  
**Tel:** 319 356 4866  
**Fax:** 319 356 7171  
**Email:** paul-mccray@uiowa.edu  
**Tissue Procurement:** Dr. M. J. Welsh, University of Iowa  
**cDNA Library Preparation:** Dr. M. Bento Soares, University of Iowa  
**cDNA Library Arrived by:** Dr. M. Bento Soares, University of Iowa  
**DNA Sequencing by:** Dr. M. Bento Soares, University of Iowa  
**Clone Distribution:** Researchers may obtain clones from Research  
**Genetics** ([www.resgen.com](http://www.resgen.com)) or from Open Biosystems  
([www.openbiosystems.com](http://www.openbiosystems.com)).  
The following repetitive elements were found in this cDNA  
sequence: 499-525 >AT rich#Low\_complexity (matched compliment)  
Seq primer: M13 FORWARD  
POLY=A yes.  
**FEATURES**  
**Source**  
1. 705  
**Location/Qualifiers**  
**organism="Homo sapiens"**  
**/mol\_type="mRNA"**  
**/db\_xref="taxon:9606"**  
**/clone="UI-CF-FNO-aff-k-13-0-UI"**  
**/tissue\_type="Human Lung Epithelial cells" (II phage resistant)"**  
**/lab\_host="DH10B (Life Technologies)"**  
**/clone\_id="UI-CF-FNO"**  
**/note="#Organ: Lung, Vector: pT73-Pac (Pharmacia) with a**  
**modified polylinker, Site 1: EcoR I; Site 2: Not I;**  
**UI-CF-FNO is a subtracted cDNA library derived from two**  
**normalized Human lung epithelial cell libraries (EN1 and**  
**DU1). The library was subtracted according to according to**  
**Bonaldo, Lennon and Soares, Genome Research, 6:791-806,**  
**1996. For additional information, contact:**  
**bento-soares@uiowa.edu**  
**TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368**  
**TAG LIB=UI-CF-FNO**  
**TAG SEQ=GACTGTGATG**  
**TAG \_SEQ=GACTGTGAGC"**  
**ORIGIN**  
**Query Match** 100.0%; Score 20; DB 14; length 705;  
**Best Local Similarity** 100.0%; Pred. No. 92;  
**Matches** 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**Oy** 1 GGTCCGAACTCATGGTGATG 20  
**Dy** 625 GGTCCGAACTCATGGTGATG 644  
**RESULT 28**  
B0772342  
**LOCUS** B0772342 748 bp mRNA linear EST 26-JUL-2002  
**DEFINITION** UT-H-EZ1-bbl-1-20-0-UT\_81 NCI CGAP Ch2 Homo sapiens cDNA clone  
**REFERENCE** UT-H-EZ1-bbl-1-20-0-UT 3', mRNA sequence.  
**ACCESSION** B0772342  
**VERSION** B0772342.1 GI:21980818

**KEYWORDS**  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 EST.  
 Home sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
 1  
 (bases 1 to 79)  
[NCI-CGAP](http://www.ncbi.nlm.nih.gov/ncicgap) http://www.ncbi.nlm.nih.gov/ncicgap.  
**AUTHORS**  
 TITLE  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
**JOURNAL**  
 COMMENT  
 Contact: Robert Strauberg, Ph. D.  
 Email: cgaps-r@mail.nih.gov  
**FEATURES**  
 Source  
**POLYA=Yes**  
**FEATURES**  
 Location/Qualifiers  
 1. 748  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_id="U1-H-EZ1-bbl1-20-0-UI"  
 /tissue\_type="Chondrosarcoma Grade II"  
 /dev\_stage="Adult"  
 /lab\_host="D110B (Life Technologies)"  
 /clone\_lib="NCI CGAP Ch2"  
 /note="Organ: Left Pelvis; Vector: PT73-Pac (Pharmacia)  
 with a modified polylinker; Site 1: Bcor I; Site 2: Not I;  
 NCI CGAP Ch2 is a normalized cDNA library containing the  
 following tissue(s): Chondrosarcoma Grade II. The library  
 was constructed according to Bonaldo, Leunon and Soares,  
 Genome Research, 6:791-806, 1996. First strand cDNA  
 synthesis was primed with an oligo-dT primer containing a  
 Not I site. Double stranded cDNA was ligated to an Bcor I  
 adaptor, digested with Not I, and cloned directionally  
 into PT73-Pac vector. The oligonucleotide used to prime  
 the synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 TAGTACCTC.  
 TAG TISSUE=grade-2-chondrosarcoma  
 TAG\_LIB=U1-H-EZ1  
 TAG\_SEQ=ATCTATAATGC"  
**ORIGIN**  
**RESULT** 29  
 BG186679/c  
**LOCUS** BG186679  
**DEFINITION** RST5654 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
**ACCESSION** BG186679  
**VERSION** BG186679.1  
**QY** 1  
 625  
**Db**  
 1 GGTCCCTACTCATGTGATG 20  
 ||||| ||||| ||||| ||||| 644  
 GGTCCCTACTCATGTGATG 644  
**KEYWORDS**  
 EST.  
 HOMEODOMAIN  
 SOURCE  
 Organism  
 Homo sapiens (human)  
**REFERENCE**  
 1  
 (bases 1 to 790)  
**KEYWORDS**  
 SOURCE  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
 1  
 (bases 1 to 790)

**AUTHORS** Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,I., Costanzo,D., McEligott,K., Boozer,S., Mayo,R., Smith,E., Veloso,N., Kika,A., Hess,J.J., Cothern,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.

**TITLE** Creation of genome-wide protein expression libraries using random activation of gene expression

**JOURNAL** Nat. Biotechnol. 19 (5), 440-445 (2001)

**MEDLINE** 11329013

**COMMENT** Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave., Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@athersys.com

**FEATURES** High quality sequence stop: 353.

**source**

1. .790  
**ORIGIN**  
*/organism="Homo sapiens"*  
*/mol\_type="mRNA"*  
*/db\_xref="taxon:9606"*  
*/cell\_line="HT1080"*  
*/clone\_id="Athersys RAGE Library"*  
*/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, those sequence tags are not necessarily expressed in HT1080 under normal circumstances."*

**RESULT** 30

**Query Match** 100.0%; Score 20; DB 12; Length 790;

**Best Local Similarity** 100.0%; Pred. No. 96; Mismatches 20;

**Matches** 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 GTTCCATACTCATGTGATG 20

**Db** 255 GGTCCATACTCATGTGATG 236

**ORIGIN**

**RESULT** 31

**Query Match** 100.0%; Score 20; DB 29; Length 809;

**Best Local Similarity** 100.0%; Pred. No. 97; Mismatches 20;

**Matches** 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 GTTCCATACTCATGTGATG 20

**Db** 743 GGTCCATACTCATGTGATG 724

**ORIGIN**

**RESULT** 31

**Query Match** 100.0%; Score 20; DB 29; Length 809;

**Best Local Similarity** 100.0%; Pred. No. 97; Mismatches 20;

**Matches** 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 GTTCCATACTCATGTGATG 20

**Db** 743 GGTCCATACTCATGTGATG 724

**ORIGIN**

**RESULT** 31

**Query Match** 100.0%; Score 20; DB 813 bp DNA linear GSS 17-DEC-2003

**DEFINITION** Homo sapiens XPA gene, VIRTUAL TRANSCRIPT, partial sequence,

**LOCUS** Homo sapiens XPA gene, VIRTUAL TRANSCRIPT, partial sequence,

**ACCESSION** AY414078

**VERSION** AY414078.1 GI:39770040

**KEYWORDS** GSS.

**SOURCE** Homo sapiens (human)

**ORGANISM** Homo sapiens (human)

**REFERENCE** Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominoidea; Homo.

**AUTHORS** 1 (bases 1 to 813)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tannenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

**TITLE** Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
*Science* 302 (5652), 1960-1963 (2003)

**JOURNAL** Science 302 (5652), 1960-1963 (2003)

**PUBLMED** 14671302

**REFERENCE** 2 (bases 1 to 813)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tannenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

**AUTHORS** 1 (bases 1 to 813)  
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tannenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

**TITLE** Direct Submission

**JOURNAL** Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

**COMMENT** This sequence was made by sequencing genomic exons and ordering them based on alignment.

**FEATURES** Location/Qualifiers

**source**

1. .813  
**ORIGIN**

**RESULT** 32

**Query Match** 100.0%; Score 20; DB 29; Length 813;

**Best Local Similarity** 100.0%; Pred. No. 97; Mismatches 20;

**Matches** 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 GTTCCATACTCATGTGATG 20

**Db** 743 GGTCCATACTCATGTGATG 724

**ORIGIN**

**RESULT** 32

**Query Match** 100.0%; Score 20; DB 873 bp mRNA linear EST 31-MAY-2003

**DEFINITION** AL545429 AL545429 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS001027YA03 5'-PRIME, mRNA sequence.

**JOURNAL** Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

**COMMENT** This sequence was made by sequencing genomic exons and ordering them based on alignment.

**FEATURES** Location/Qualifiers

	ACCESSION	AL545429	FEATURES	High quality sequence stop: 662.
	VERSION	AL545429.2	SOURCE	Alt Location/Qualifiers
	KEYWORDS			1..1059
	AUTHORS			/organism="Homo sapiens"
	TITLE	Homo sapiens (human)		/mol_type="mRNA"
	JOURNAL			/db_xref="taxon:606"
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 873) Li, W.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 15, 2001 this sequence version replaced gi:12877910. Contact: Genoscope - Centre National de Sequencage			/clone="IMAGE:553943"
FEATURES	source	BP 191 9106 EVRY cedex - France		/tissue_type="telomysarcoma"
		Email: segr@genoscope.cns.fr. Web : www.genoscope.cns.fr		/lab_host="DH10B (phage-resistant)"
		Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4910.r For more information about thi cluster, see		/clone_lib="NIH MCC_71"
		http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1027A02QNP1&cluster=4910.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0D1027A02QNP1.		/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Location/Qualifiers
		1..873 /organism="Homo sapiens"		Average insert size 2.1 kb."
		/mol_type="mRNA"		
		/db_xref="taxon:9606"		
		/clone="CS0D1027YA03"		
		/tissue_type="PLACENTA COT 25-NORMALIZED"		
		/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"		
		/note="1st strand cDNA was primed with a NotI-oligo (5') primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMSPORT 6 vector. Library was normalized."		
ORIGIN				
RESULT	33		RESULT	34
BM468458/c			AL573331	AL573331
DEFINITION			AL573331	AL573331
Best Local Similarity	100.0%	Score 20; DB 9; Length 873;	100.0%; Score 20; DB 12; Length 1059;	Query Match
Matches	20;	Pred. No. 1.e+02; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;	LOCUS
Qy	1	GGTCATACTCATGTGATG 20	AL573331	AL573331
Db	809	GGTCATACTCATGTGATG 790	743	743
VERSION				
KEYWORDS				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1114) Li, W.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On Feb 16, 2001 this sequence version replaced gi:12932473. Contact: Genoscope - Centre National de Sequencage			
FEATURES	source	BP 191 9106 EVRY cedex - France		
		Email: segr@genoscope.cns.fr		
		Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4910.r For more information about thi cluster, see		
		http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0D1042AB02NP1&cluster=4910.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0D1042AB02NP1.		
		1..1114 /organism="Homo sapiens"		
		/mol_type="mRNA"		
		/db_xref="taxon:9606"		
		/clone="CS0D1042YC03"		
		/tissue_type="PLACENTA COT 25-NORMALIZED"		
		/clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"		
		/note="1st strand cDNA was primed with a NotI-oligo (5') primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMSPORT 6 vector. Library was normalized."		
ORIGIN				
RESULT	33		Query Match	100.0%; Score 20; DB 9; Length 1114;
BM468458			Best Local Similarity	100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;
DEFINITION			Matches	
Best Local Similarity	100.0%	Score 20; DB 9; Length 873;	100.0%; Score 20; DB 12; Length 1059;	
Matches	20;	Pred. No. 1.e+02; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	GGTCATACTCATGTGATG 20	Qy	1
Db	809	GGTCATACTCATGTGATG 790	Db	1
VERSION				
KEYWORDS				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
COMMENT	Eukaryota; Bacteria; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1059) NIH-MGC http://mgc.ncbi.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgsb@r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLNL12224 row: J column: 04			

Db	559	GTCCTAATCTCATGTTGATG	578
RESULT	35		
AL54961/c	AL54961	Homo sapiens	1129 bp mRNA linear EST 31-MAY-2003
DEFINITION		PLACENTA COT 25-NORMALIZED	Homo sapiens cDNA
LOCUS	AL54961	Clone CSOD1042YC03	5'-PRIME, mRNA sequence.
ACCESSION	AL54961		
VERSION	AL54961.2	GI:31270783	
KEYWORDS	EST.		
SOURCE			
ORGANISM		Homo sapiens (human)	
FEATURES			
SOURCE			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1	(bases 1 to 1129)	
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polajes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On Feb 15, 2001 this sequence version replaced gi:12884484.		
FEATURES			
SOURCE			
Genoscope - Centre National de Sequencage			
BP 191 91006 EVRY cedex - France			
Email: segr@genoscope.cns.fr			
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4910.r For more information about this cluster, see			
<a href="http://www.genoscope.cns.fr/cgi-bin/clcluster.cgi?seq=CSOD1042AB02QPI&amp;cluster=4910.r">http://www.genoscope.cns.fr/cgi-bin/clcluster.cgi?seq=CSOD1042AB02QPI&amp;cluster=4910.r</a> . Contact : Feng Liang Email: <a href="mailto:fliang@lifetech.com">fliang@lifetech.com</a> URL : <a href="http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODM002CC12NPI">http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODM002CC12NPI</a> .			
ORIGIN			
FEATURES			
SOURCE			
1. 1123			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
/clone="CSOD1042YC03"			
/tissue type="PLACENTA COT 25-NORMALIZED"			
/clone Lib="Homo sapiens PLACENTA COT 25-NORMALIZED"			
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pEMSPORT 6 vector. Library was normalized."			
ORIGIN			
FEATURES			
SOURCE			
Quary Match	100.0%	Score 20; DB 9; Length 1129;	
Best Local Similarity	100.0%	Pred. No. 1.1e+02;	
Matches	20;	Conservative	
Qy	1	GTCCTAATCTCATGTTGATG	20
Db	818	GGTCCTAATCTCATGTTGATG	799
RESULT	37		
AL531628	AL531628	1201 bp mRNA linear EST 23-MAY-2003	
LOCUS			
DEFINITION			
CSDM002CC12NPI			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM		Homo sapiens (human)	
FEATURES			
SOURCE			
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1	(bases 1 to 1201)	
AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polajes,D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	On Feb 13, 2001 this sequence version replaced gi:12795121.		
FEATURES			
SOURCE			
Genoscope - Centre National de Sequencage			
BP 191 91006 EVRY cedex - France			
Email: segr@genoscope.cns.fr			
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4910.r For more information about this cluster, see			
<a href="http://www.genoscope.cns.fr/cgi-bin/clcluster.cgi?seq=CSODM002CC12NPI&amp;cluster=4910.r">http://www.genoscope.cns.fr/cgi-bin/clcluster.cgi?seq=CSODM002CC12NPI&amp;cluster=4910.r</a> . Contact : Feng Liang Email: <a href="mailto:fliang@lifetech.com">fliang@lifetech.com</a> URL : <a href="http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODM002CC12NPI">http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODM002CC12NPI</a> .			
FEATURES			
SOURCE			
1. 1201			



RESULT 40	BQ321319/c	568 bp	mRNA	linear	EST 17-MAY-2002	REFERENCE	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
LOCUS	BQ321319	1	(bases 1 to 625)			AUTHORS	Kitayama,A., Ierasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.
DEFINITION	QV4-CT0491-080800-341-a11 Ctr0491	Homo Sapiens cDNA, mRNA sequence.				TITLE	Expressed genes in X. laevis embryo
ACCESSION	BQ321319					JOURNAL	Unpublished (2001)
VERSION	BQ321319.1	GI:20929303				COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information
KEYWORDS	EST.						National Institute of Genetics, Japan
SOURCE	Homo sapiens						111 Yata, Mishima, Shizuoka 411-8540, Japan
ORGANISM	Homo sapiens (human)						Tel: 81-559-81-6856
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.						Fax: 81-559-81-6855
AUTHORS	Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordim,S., Costa,F.F., Goldmann,G.H., Carvalho,A.P., Mattukuma,A., Bajic,G.S., Simpson,D.H., Brunein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.						Email: tshini@genes.nig.ac.jp
COMMENT	Laboratory of Cancer Genetics						The information of this clone is available through the following URL.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags						<a href="http://xenopus.nibb.ac.jp/">http://xenopus.nibb.ac.jp/</a>
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)						
MEDLINE	20020663						
PUBMED	10737800						
CONTACT	Simpson A.J.G.						
	Ludwig Institute for Cancer Research						
	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil						
TEL	+55-11-2704922						
FAX	+55-11-2707001						
EMAIL	asimpson@ludwig.org.br						
	This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL ( <a href="http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV4&amp;t2=QV4-CT0491-080800-341-a11&amp;t3=2000-08-08&amp;t4=1">http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV4&amp;t2=QV4-CT0491-080800-341-a11&amp;t3=2000-08-08&amp;t4=1</a> )						
Seq primer	puc 18 forward						
High quality sequence stop:	45.						
FEATURES	Location/Qualifiers						
SOURCE	1. 568						
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	/def_stage="Adult"						
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	/note="Organ: colon; Vector: puc18; Site_1: Smal; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."						
ORIGIN							
Query Match	92.0%	Score	18.4;	DB	12;	Length	625;
Best Local Similarity	95.0%	Pred.	No.	4.9e+02;			
Matches	19;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps							0;
Db	49						
FEATURES	Source						
ORIGIN							
RESULT 42	A1634902	711 bp	mRNA	linear	EST 26-APR-1999	Query Match	92.0%
LOCUS	A1634902	711	cDNA clone IMAGE:2294106 3'			Best Local Similarity	95.0%
DEFINITION	A1634902	x11	NCI CGAP Panel Homo sapiens cDNA clone IMAGE:2294106 3'			Pred.	No. 4.9e+02;
			(HUMAN); mRNA Sequence.			Mismatches	1;
VERSION	A1634902.1					Indels	0;
KEYWORDS	EST.					Gaps	0;
SOURCE							
ORGANISM	Homo sapiens (human)						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.						
REFERENCE							
AUTHORS	1 (bases 1 to 711)						
JOURNAL	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .						
COMMENT	Tumor Gene Index						
	Unpublished (1997)						
	Contact: Robert Strausberg, Ph.D.						
	Email: cgaps@mail.nih.gov						
	Life Technologies catalog #:						
	11548-013						
	DNA Sequencing by: Washington University Genome Sequencing Center						
	Clone distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <a href="http://www-bio-lnl.gov/bbrp/image/image.html">www-bio-lnl.gov/bbrp/image/image.html</a>						
	Seq primer: -40UP from Gibco						
FEATURES	Location/Qualifiers						
SOURCE	1. .711						
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	/tissue type="adenocarcinoma"						
	/lab_host="DH10B"						

clone CS0DI027YA03 3'-PRIME, mRNA sequence.

/clone lib="Nci\_CGAP\_Pan1"  
 /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Sall;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"

**ORIGIN**

Query Match 92.0%; Score 18.4; DB 9; Length 711;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTGATG 20  
 Db 602 GGGCCATACTCATGTGATG 199

**RESULT 43**

LOCUS BG187563 854 bp mRNA linear EST 21-APR-2001  
 DEFINITION RST6691 Athersys RAGE library Homo sapiens cDNA, mRNA sequence.  
 VERSION BG187563.1 GI:13709378  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE**  
 1 (bases 1 to 854)  
**AUTHORS** Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., Mcelligott,K., Boozer,S., May,B., Smith,E., Veloso,N., Kilkka,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Duan,M.  
**TITLE** Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)  
**JOURNAL** MEDLINE 21227151  
**PUBLMED** 11329013  
**COMMENT** Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scain@athersys.com  
**FEATURES**  
**SOURCE**

High quality sequence stop: 482.  
 Location/Qualifiers

1. -854  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and BcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

**ORIGIN**

Query Match 92.0%; Score 18.4; DB 9; Length 857;  
 Best Local Similarity 95.0%; Pred. No. 5.6e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCCATACTCATGTGATG 20  
 Db 588 GGTCCATACTCATGTGATG 607

**RESULT 45**

LOCUS CC448351 1024 bp DNA linear GSS 22-MAY-2003  
 DEFINITION ZMMBBC0122P17r ZMMBBC Zea mays subsp. mays genomic clone  
 VERSION CC448351.1 GI:30995914  
 KEYWORDS GSS.  
 SOURCE Zea mays subsp. mays (maize)  
 ORGANISM Zea mays subsp. mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
**REFERENCE**  
 1 (bases 1 to 1024)  
**AUTHORS** Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C., Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.  
**TITLE** Sequencing of the maize genome at PGRI (2003b)  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Bharti,A.K.  
 Dr.Joachim Messing's lab  
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University  
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 Tel: 732 445 3801  
 Fax: 732 445 5735

**RESULT 44**

LOCUS AL571156 857 bp mRNA linear EST 31-MAY-2003  
 DEFINITION AL571156 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

Email: bharti@waksman.rutgers.edu

**FEATURES**      **SOURCE**      **High quality sequence start: 66.**  
**Class: BAC ends**  
**Location/Qualifiers**      1..1024

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Query Match Similarity: 92.0%; Score 18.4; DB 28; Length 1024;

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/dev_stage="unfertilized egg"
/lab_host="DH10B"
/clone_lab="Blackshear/Soares normalized Xenopus egg
/note="Vector: PT773-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
PT773-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery.' Genome Research
6:711-806, 1996. The first strand synthesis used a
NotI-dT18 primer; double stranded cDNAs were ligated to
EcoRI adaptors digested with NotI, and directionally
cloned into the NotI and EcoRI-digested PT773-Pac vector.
The library contained approximately 7.2 x 105
recombinants, with average insert sizes of 1-1.5 kb. "

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Oy	1	GTCCTACTCATGTGATG	20
Db	759	GGTCATTCATGTGATG	778

AW646323 AW646323 linear EST 26-APR-2001

**Locus** AW646323      **Accession** AW646323  
**Definition** Blackshear/Soares normalized cDNA clone PBX0162E10 5', mRNA sequence.  
**Linearity** Linear      **Format** EBI 26-APR-2001  
**Length** 420 bp      **Organism** Xenopus laevis  
**Source** Egg library Xenopus laevis

**KEYWORD** EST.  
**SOURCE** Xenopus laevis (African clawed frog)  
**ORGANISM** Xenopus laevis

**AUTHORS** Blackstone, P.J., Ball, W.S., Inorn, J.M., Kemington, E.A., Scarpa, N.G., Jr., Moore, D.T., Bouffard, G. M., Beckmann-Sternberg, S.M., Touchman, J.W., Bonaldo, M.F. and Soares, M.B.

LITTLE  
THE NIHS XENOPUS MATERNAL BSI PROJECT: INTERIM ANALYSIS OF THE  
FIRST 13,879 ESTS FROM UNFERTILIZED EGGS  
JOURNAL  
Gene 267 (1), 71-87 (2001)  
MEDLINE  
21211403  
PUBMED  
11311557  
COMMENT  
Contact: Perry J. Blackshear

Office of Clinical Research and Laboratory of Signal Transduction  
National Institute of Environmental Health Sciences  
A2-105 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,  
USA

Tel: 919 541-4899  
Fax: 919 541-4571  
Email: black09@niehs.nih.gov  
Clone is available through Research Genetics, Inc., 2130 Memorial Parkway, Huntsville, AL 35901

phone 800-533-4363 ext. cdna, fax 256-536-9016 att:cdna, email cdnaregen.com  
DNA Sequencing and analyses performed by National Institutes of Health Intramural sequencing Center (NISC).  
PCR Primer: TGTAAACGAGCCGCT  
FORWARD: TGTAAACGAGCCGCT  
BACKWARD: CAGGAACACCTATGACC  
Plate: 052 row: B column: 10  
Seq primer: T7 primer.

FEATURES	Location/Qualifiers
SOURCE	
1. .420	

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/mol type="mRNA"
/db_xref="taxon:8355"
/clone="PBX0162E10"
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QY	1	GCTCCATACTCTGTTGATG	20	REFERENCE 1 (bases 1 to 828)
Db	429	GGTCATCATCTCTGTGNG	448	AUTHORS Lai, J., Dey, N., Kim, C.-S., Becroft, P., Larkins, B., Linton, E. and Messing, J.
				TITLE Sequencing of the maize endosperm ESTs
RESULT	48			JOURNAL Unpublished (2002)
AL637062/c				COMMENT Contact: Lai, Jinsheng Dr. Joachim Messing's lab Watman Institute, Rutgers University 190 Frelinghuysen Rd., Piscataway, NJ 08854, USA Tel: 732-445-3801 Fax: 732-445-5735
LOCUS	AL637062	587 bp	mRNA	REFERENCE mRNA sequence.
DEFINITION	AL637062	XGC-neurula	Silurana tropicalis	AUTHORS Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
ACCESSION	AL637062	cDNA clone TNeu003d20	EST	TITLE Unpublished (2003)
VERSION	AL637062.2	5'		JOURNAL On Nov 7, 2001 this sequence version replaced gi:16789041.
KEYWORDS				COMMENT Contact: Huckie E Sanger Institute Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk
SOURCE				This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn. cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end. Vector: pCS107; Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B
COMMENT				Sanger Xenopus tropicalis EST Project 2001 TROPICALIS_SEQUENCE_ID: TNeu003d20.p1ksp6 SEQUENCING_PRIMER: SP6 FEATURES source Sequencing_Location/Qualifiers
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ORIGIN				COMMENT Contact: Robert Straubenberg, Ph.D. Email: cgaps@mail.nih.gov Tissue Procurement: ATCC cDNA library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLM at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: L1AM1270 row: J column: 20 High quality sequence start: 63 High quality sequence stop: 173. Location/Qualifiers
RESULT	49			FEATURES source Sequencing_Location/Qualifiers
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DEFINITION	EL01032A02.b	Endosperm	Zea mays	QY
ACCESSION	CD434346	3	mRNA	2
VERSION	CD434346.1	GT:31349989	linear	EST
KEYWORDS				Db
SOURCE				zea mays
ORGANISM				Bukaryota; Viridiplantae; Streptophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.4 kb. Library prepared by Life  
Technologies.

ORIGIN

Query Match 85.0%; Score 17; DB 12; Length 808;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GTCCTAATCTGTGTA 18  
Db 48 GTCCTAATCTGTGTA 64

Search completed: August 17, 2004, 15:45:29  
Job time : 2606 secs

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